

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:15:55 ; Search time 30 Seconds  
(without alignments)  
579.659 Million cell updates/sec

Title: US-10-052-798-1  
Perfect score: 2169  
Sequence: 1 MEORGONAPASGARRKRRGP.....HLSSGKMYLEGNADSAXS 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfillseq1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2167	99.9	411	3	US-09-329-633A-2
2	2167	99.9	411	4	US-09-079-029-1
3	2163	99.7	411	4	US-09-134-618-2
4	2160	99.6	411	4	US-10-039-785-3
5	2152	99.2	412	4	US-09-333-593A-2
6	2135.5	98.5	440	3	US-08-883-036A-2
7	2135.5	98.5	440	3	US-09-336-201-2
8	1610.5	74.3	350	4	US-09-134-618-6
9	1597	73.6	303	4	US-09-333-593A-2
10	1072	49.4	468	4	US-09-013-895A-4
11	1072	49.4	468	4	US-09-565-918-2
12	1072	49.4	468	4	US-09-448-868-2
13	1072	49.4	468	4	US-10-039-785-1
14	1061.5	48.9	467	3	US-09-086-483A-6
15	1061.5	48.9	467	4	US-09-580-212-6
16	996	45.9	424	4	US-09-333-593A-8
17	819.5	37.8	386	4	US-09-086-483A-2
18	819.5	37.8	386	4	US-09-580-212-2
19	819.5	37.8	386	4	US-10-039-785-4
20	811.5	37.4	386	4	US-09-130-491-6
21	522	24.1	234	4	US-09-130-491-12
22	463	21.3	368	2	US-08-651-579-2
23	398.5	18.4	299	3	US-09-133-927-3
24	398.5	18.4	299	4	US-09-134-618-4
25	398.5	18.4	299	4	US-10-039-785-2
26	379.5	17.5	259	3	US-09-006-353A-2
27	379.5	17.5	259	4	US-09-573-986-2

28	342	15.8	67	4	US-09-527-236A-26	Sequence 26, Appl
29	264.5	12.2	471	4	US-09-513-007-2	Sequence 2, Appl
30	262	12.1	51	3	US-08-883-036A-4	Sequence 4, Appl
31	262	12.1	51	4	US-09-536-201-4	Sequence 4, Appl
32	218	10.1	67	4	US-09-527-236A-25	Sequence 25, Appl
33	214	9.9	453	3	US-09-086-483A-5	Sequence 5, Appl
34	214	9.9	453	4	US-09-580-212-5	Sequence 25, Appl
35	210.5	9.7	455	1	US-08-050-319B-25	Sequence 25, Appl
36	210.5	9.7	455	1	US-08-321-668-2	Sequence 2, Appl
37	210.5	9.7	455	1	US-08-837-941-2	Sequence 2, Appl
38	210.5	9.7	455	2	US-08-126-016-2	Sequence 2, Appl
39	210.5	9.7	455	2	US-08-465-982-25	Sequence 25, Appl
40	210.5	9.7	455	3	US-08-815-469-5	Sequence 5, Appl
41	210.5	9.7	455	3	US-09-006-353A-3	Sequence 3, Appl
42	210.5	9.7	455	4	US-09-527-236A-5	Sequence 5, Appl
43	210.5	9.7	455	4	US-08-054-970-2	Sequence 2, Appl
44	210.5	9.7	455	4	US-09-565-918-4	Sequence 4, Appl
45	210.5	9.7	455	4	US-09-573-986-3	Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-329-633A-2  
Sequence 2, Application US/09329633A  
Patent No. 6252050  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntarapai, Ajan  
TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND  
TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD  
FILE REFERENCE: P14681 (REVISED)  
CURRENT FILING DATE: 1999-06-10  
PRIORITY FILING DATE: 1999-06-10  
PRIOR APPLICATION NUMBER: US 60/089,253  
NUMBER OF SEQ ID NOS: 2  
SEQ ID NO 2  
LENGTH: 411  
TYPE: PRT  
ORGANISM: human  
FEATURE:  
NAME/KEY: xaa  
LOCATION: 410  
OTHER INFORMATION: xaa = leu or met  
US-09-329-633A-2

Query Match 99.9% Score 2167, DB 3: Length 411;  
Best Local Similarity 100.0% Pred. No. 5.6e-198;

Matches, 411: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEORGONAPASGARRKRRGP	PREARGARPLRYPKTLVVAVALLVLSAESALITQOD	60
DB	1	MEORGONAPASGARRKRRGP	PREARGARPLRYPKTLVVAVALLVLSAESALITQOD	60
QY	61	LAPQORAPQOKRSSPSEGLCP	PGHHITSEDRDCTSCYGGDYSTHWNDDLFCILCTKCD	120
DB	61	LAPQORAPQOKRSSPSEGLCP	PGHHITSEDRDCTSCYGGDYSTHWNDDLFCILCTKCD	120
QY	121	SGEVELSPCTTRNTVOCCEGT	FRREDSPEMKCRKCRGCVKVDCTPMWDIECVH	180
DB	121	SGEVELSPCTTRNTVOCCEGT	FRREDSPEMKCRKCRGCVKVDCTPMWDIECVH	180
QY	181	KESGIITGVVAAVLVAVFCK	SLMKKVLPLKIGISGGGDPERVDSSORPGAED	240
DB	181	KESGIITGVVAAVLVAVFCK	SLMKKVLPLKIGISGGGDPERVDSSORPGAED	240
QY	241	NVLNEIYSITLPTQVPEQEM	EVQBPAPFTGVNMLSPGSEHLLPAPAEARSQRRLLVPA	300
DB	241	NVLNEIYSITLPTQVPEQEM	EVQBPAPFTGVNMLSPGSEHLLPAPAEARSQRRLLVPA	300

QY 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360  
DB 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360  
QY 361 VNKGRDASVHTLLDALETTGELRLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
DB 361 VNKGRDASVHTLLDALETTGELRLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

## RESULT 2

US-09-079-029-1  
Sequence 1, Application US/09079029  
Patent No. 6342369

## GENERAL INFORMATION:

APPLICANT: Adams, Camilla W.  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntcharapai, Anan  
APPLICANT: Kim, Kyung J.  
TITLE OF INVENTION: Apo-2 Receptor  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatlin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079, 029

## FILING DATE:

CLASSIFICATION:

## ATTORNEY/AGENT INFORMATION:

NAME: Maichang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P1101R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 411 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-079-029-1

Query Match 99.9%; Score 2167; DB 4; Length 411;  
Best Local Similarity 100.0%; Pred. No. 5,6e-198;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQGNAPASGARKRHPGPREARPGARPELRYPKTLVVAVALLVSAESALITQOD 60  
DB 1 MEQGNAPASGARKRHPGPREARPGARPELRYPKTLVVAVALLVSAESALITQOD 60  
QY 61 LAPQORAPPOOKRSPSEGLCPGPHHISEDGRDCISCKYGGDYSTHNNDLFLCRLCTRC 120  
DB 61 LAPQORAPPOOKRSPSEGLCPGPHHISEDGRDCISCKYGGDYSTHNNDLFLCRLCTRC 120  
QY 121 SGEVELSPCTTTNTVCCCEGTFRREDSPEMCRKCRTPGKAVKVGDCITPMSDIECVH 180  
DB 121 SGEVELSPCTTTNTVCCCEGTFRREDSPEMCRKCRTPGKAVKVGDCITPMSDIECVH 180  
QY 181 KESGIIIGVYAAVVAVAVFVCKSLMKKVPYLKIGICSGGGDPERVDRSSORPGAED 240  
DB 181 KESGIIIGVYAAVVAVAVFVCKSLMKKVPYLKIGICSGGGDPERVDRSSORPGAED 240  
QY 241 NVLNEIVSILOPVOPEQEMEVQEPAPETGVNMLSPGSEHLLPAAEARSQRRLVPA 300  
DB 241 NVLNEIVSILOPVOPEQEMEVQEPAPETGVNMLSPGSEHLLPAAEARSQRRLVPA 300

QY 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360  
DB 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360  
QY 361 VNKGRDASVHTLLDALETTGELRLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
DB 361 VNKGRDASVHTLLDALETTGELRLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

## RESULT 3

US-09-134-618-2

Sequence 2, Application US/09134618  
Patent No. 6417328

## GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.  
TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND  
FILE REFERENCE: 480140.432  
CURRENT APPLICATION NUMBER: US/09/134, 618  
CURRENT FILING DATE: 1998-08-14  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-134-618-2

Query Match 99.7%; Score 2163; DB 4; Length 411;  
Best Local Similarity 99.5%; Pred. No. 1.4e-197;  
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEQGNAPASGARKRHPGPREARPGARPELRYPKTLVVAVALLVSAESALITQOD 60  
DB 1 MEQGNAPASGARKRHPGPREARPGARPELRYPKTLVVAVALLVSAESALITQOD 60  
QY 61 LAPQORAPPOOKRSPSEGLCPGPHHISEDGRDCISCKYGGDYSTHNNDLFLCRLCTRC 120  
DB 61 LAPQORAPPOOKRSPSEGLCPGPHHISEDGRDCISCKYGGDYSTHNNDLFLCRLCTRC 120  
QY 121 SGEVELSPCTTTNTVCCCEGTFRREDSPEMCRKCRTPGKAVKVGDCITPMSDIECVH 180  
DB 121 SGEVELSPCTTTNTVCCCEGTFRREDSPEMCRKCRTPGKAVKVGDCITPMSDIECVH 180  
QY 181 KESGIIIGVYAAVVAVAVFVCKSLMKKVPYLKIGICSGGGDPERVDRSSORPGAED 240  
DB 181 KESGIIIGVYAAVVAVAVFVCKSLMKKVPYLKIGICSGGGDPERVDRSSORPGAED 240  
QY 241 NVLNEIVSILOPVOPEQEMEVQEPAPETGVNMLSPGSEHLLPAAEARSQRRLVPA 300  
DB 241 NVLNEIVSILOPVOPEQEMEVQEPAPETGVNMLSPGSEHLLPAAEARSQRRLVPA 300  
QY 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360  
DB 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360  
QY 361 VNKGRDASVHTLLDALETTGELRLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
DB 361 VNKGRDASVHTLLDALETTGELRLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

## RESULT 4

US-10-039-785-3

Sequence 3, Application US/10039785  
Patent No. 6538938

## GENERAL INFORMATION:

APPLICANT: Salcedo et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
FILE REFERENCE: PF550  
CURRENT APPLICATION NUMBER: US/10/039, 785  
CURRENT FILING DATE: 2002-05-07

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: PRIOR APPLICATION NUMBER: 60/369,860
: PRIOR FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: 60/341,237
: PRIOR FILING DATE: 2001-12-20
: PRIOR APPLICATION NUMBER: 60/331,310
: PRIOR FILING DATE: 2001-11-14
: PRIOR APPLICATION NUMBER: 60/331,044
: PRIOR FILING DATE: 2001-11-07
: PRIOR APPLICATION NUMBER: 60/327,364
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/323,807
: PRIOR FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: 60/309,176
: PRIOR FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: 60/294,981
: PRIOR FILING DATE: 2001-06-04
: PRIOR APPLICATION NUMBER: 60/293,473
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-039-785-3

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Query Match      99.6%; Score 2160; DB 4; Length 411;
Best Local Similarity 99.3%; Pred. No. 2,6e-197;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MEORGNAPASGARKRHGPGPREARGARPGRLVPTLVVAVALLVSAESALITQOD 60
D 1 MEORGNAPASGARKRHGPGPREARGARPGRLVPTLVVAVALLVSAESALITQOD 60
QY 61 LAPQORAPPOOKRSSPSEGLCPRGHHSSEGRDCISCKYGODYSTHNNDLFLCRLCTRC 120
D 61 LAPQORAPPOOKRSSPSEGLCPRGHHSSEGRDCISCKYGODYSTHNNDLFLCRLCTRC 120
QY 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCKKCTGCRGVKVGDDCTPMSDIECVH 180
D 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCKKCTGCRGVKVGDDCTPMSDIECVH 180
QY 181 KESGIIIGVYAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGDPRVDRSSORPAGD 240
D 181 KESGIIIGVYAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGDPRVDRSSORPAGD 240
QY 241 NVLNEIVSILOPTQVPOEMEVOEPAPPTGVNMLSPGESEHLLPAPAEERSQRRLLVPA 300
D 241 NVLNEIVSILOPTQVPOEMEVOEPAPPTGVNMLSPGESEHLLPAPAEERSQRRLLVPA 300
QY 301 NEGDPETLROCFDADFVDFDSWEPMLMKRLGLMNDIEIKVAKAEAGHRDTLYTMLIKW 360
D 301 NEGDPETLROCFDADFVDFDSWEPMLMKRLGLMNDIEIKVAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTGRDASVHTLLDALETIGERLAKOKIEDHLSSGKFMYLEGNADSAMS 411
D 361 VNKTGRDASVHTLLDALETIGERLAKOKIEDHLSSGKFMYLEGNADSAMS 411

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RESULT 5
US-09-333-593A-2
: Sequence 2, Application US/09333593A
: Patent No. 6313269
: GENERAL INFORMATION:
: APPLICANT: DEEN, KEITH C.
: APPLICANT: YOUNG, PETER R.
: APPLICANT: MARSHALL, LISA A.
: APPLICANT: ROSHAK, AMY K.
: APPLICANT: TAN, KONG B.
: APPLICANT: TRUENH, ALEMSGED
: TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
: FILE REFERENCE: GH-50008-2

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: CURRENT APPLICATION NUMBER: US/09/333,593A
: CURRENT FILING DATE: 1999-06-15
: PRIOR APPLICATION NUMBER: 08/916,625
: PRIOR FILING DATE: 1997-08-22
: PRIOR APPLICATION NUMBER: 08/953,684
: PRIOR FILING DATE: 1997-05-09
: PRIOR APPLICATION NUMBER: 60/041,230
: PRIOR FILING DATE: 1997-03-14
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 412
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
US-09-333-593A-2

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Query Match      99.2%; Score 2152; DB 4; Length 412;
Best Local Similarity 99.3%; Pred. No. 1.5e-196;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MEORGNAPASGARKRHGPGPREARGARPGRLVPTLVVAVALLVSAESALITQOD 60
D 1 MEORGNAPASGARKRHGPGPREARGARPGRLVPTLVVAVALLVSAESALITQOD 60
QY 61 LAPQORAPPOOKRSSPSEGLCPRGHHSSEGRDCISCKYGODYSTHNNDLFLCRLCTRC 120
D 61 LAPQORAPPOOKRSSPSEGLCPRGHHSSEGRDCISCKYGODYSTHNNDLFLCRLCTRC 120
QY 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCKKCTGCRGVKVGDDCTPMSDIECVH 180
D 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCKKCTGCRGVKVGDDCTPMSDIECVH 180
QY 181 KESGIIIGVYAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGDPRVDRSSORPAGD 240
D 181 KESGIIIGVYAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGDPRVDRSSORPAGD 240
QY 241 NVLNEIVSILOPTQVPOEMEVOEPAPPTGVNMLSPGESEHLLPAPAEERSQRRLLVPA 300
D 241 NVLNEIVSILOPTQVPOEMEVOEPAPPTGVNMLSPGESEHLLPAPAEERSQRRLLVPA 300
QY 301 NEGDPETLROCFDADFVDFDSWEPMLMKRLGLMNDIEIKVAKAEAGHRDTLYTMLIKW 360
D 301 NEGDPETLROCFDADFVDFDSWEPMLMKRLGLMNDIEIKVAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTGRDASVHTLLDALETIGERLAKOKIEDHLSSGKFMYLEGNADSAMS 411
D 361 VNKTGRDASVHTLLDALETIGERLAKOKIEDHLSSGKFMYLEGNADSAMS 411

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RESULT 6
US-08-883-036A-2
: Sequence 2, Application US/08883036A
: Patent No. 6072047
: GENERAL INFORMATION:
: APPLICANT: Rauch, Charles
: APPLICANT: Malczak, Henning
: TITLE OF INVENTION: Receptor That Binds TRAIL
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle,
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: Macintosh 7.6
: SOFTWARE: Microsoft Word, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/883,036A
: FILING DATE: 26-JUN-1997

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CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US --to be assigned--  
FILING DATE: 04-JUN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/829,536  
FILING DATE: 28-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/815,255  
FILING DATE: 12-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/799,861  
FILING DATE: 13-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2625-D  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-883-036A-2

Query Match 98.5%; Score 2135.5; DB 3; Length 440;  
Best Local Similarity 93.0%; Pred. No. 6.2e-195;  
Matches 409; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

QY 1 MEORGNAPASGARKRHGPGREARGLRVKPTLVVAAVLLVSAESALITQOD 60  
DB 1 MEORGNAPASGARKRHGPGREARGLRVKPTLVVAAVLLVSAESALITQOD 60  
QY 61 LAPOORAPPOOKRSSPSGGLCPGPHHISEDGRDCISCKYGODYSTHNDLLFCLRCTCD 120  
DB 61 LAPOORAPPOOKRSSPSGGLCPGPHHISEDGRDCISCKYGODYSTHNDLLFCLRCTCD 120  
QY 121 SGEVELSPCTTTRNTVCCCEGTREEDSPCMCKRCRTGCPRGVAVGDDCTPMSDIECVH 180  
DB 121 SGEVELSPCTTTRNTVCCCEGTREEDSPCMCKRCRTGCPRGVAVGDDCTPMSDIECVH 180  
QY 181 KE-----SGIIIGVTAAVVLIYAVFCKSLMKV 211  
DB 181 KESGTHSGEAPAVEETVTSPPGPASPCLSGIIIGVTAAVVLIYAVFCKSLMKV 240  
QY 212 LPYLKIGISGGGDPERVDSSQRPAGADNVNLNETVSILOPTQVPEOEMEYOEPABPTGV 271  
DB 241 LPYLKIGISGGGDPERVDSSQRPAGADNVNLNETVSILOPTQVPEOEMEYOEPABPTGV 300  
QY 272 NMLSPGSEHLLPEAEERSQRRLVLANEGDPTETLRQCFDFADLVFPDSMEPLMKV 331  
DB 301 NMLSPGSEHLLPEAEERSQRRLVLANEGDPTETLRQCFDFADLVFPDSMEPLMKV 360  
QY 332 LGLNDNETKYAKAAGHRTLYMLIKVWKTKGRDASVHTLLDALETGLRLAKOKIED 391  
DB 361 LGLNDNETKYAKAAGHRTLYMLIKVWKTKGRDASVHTLLDALETGLRLAKOKIED 420  
QY 392 HLSSGKFMYLEGNADSAXS 411  
DB 421 HLSSGKFMYLEGNADSAXS 440

RESULT 7  
US-09-536-201-2  
Sequence 2, Application us/09536201  
Patent No. 6569642  
GENERAL INFORMATION:  
APPLICANT: Rauch, Charles  
APPLICANT: Walczak, Henning

TITLE OF INVENTION: Receptor That Blinds TRAIL  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle,  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Macintosh 7.6  
SOFTWARE: Microsoft Word, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/536,201  
FILING DATE: 27-MAR-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/883,036  
FILING DATE: 26-JUN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US --to be assigned--  
FILING DATE: 04-JUN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/829,536  
FILING DATE: 28-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/815,255  
FILING DATE: 12-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/799,861  
FILING DATE: 13-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2625-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-536-201-2

Query Match 98.5%; Score 2135.5; DB 4; Length 440;  
Best Local Similarity 93.0%; Pred. No. 6.2e-195;  
Matches 409; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

QY 1 MEORGNAPASGARKRHGPGREARGLRVKPTLVVAAVLLVSAESALITQOD 60  
DB 1 MEORGNAPASGARKRHGPGREARGLRVKPTLVVAAVLLVSAESALITQOD 60  
QY 61 LAPOORAPPOOKRSSPSGGLCPGPHHISEDGRDCISCKYGODYSTHNDLLFCLRCTCD 120  
DB 61 LAPOORAPPOOKRSSPSGGLCPGPHHISEDGRDCISCKYGODYSTHNDLLFCLRCTCD 120  
QY 121 SGEVELSPCTTTRNTVCCCEGTREEDSPCMCKRCRTGCPRGVAVGDDCTPMSDIECVH 180  
DB 121 SGEVELSPCTTTRNTVCCCEGTREEDSPCMCKRCRTGCPRGVAVGDDCTPMSDIECVH 180  
QY 181 KE-----SGIIIGVTAAVVLIYAVFCKSLMKV 211  
DB 181 KESGTHSGEAPAVEETVTSPPGPASPCLSGIIIGVTAAVVLIYAVFCKSLMKV 240  
QY 212 LPYLKIGISGGGDPERVDSSQRPAGADNVNLNETVSILOPTQVPEOEMEYOEPABPTGV 271  
DB 241 LPYLKIGISGGGDPERVDSSQRPAGADNVNLNETVSILOPTQVPEOEMEYOEPABPTGV 300





STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/013,895A  
FILING DATE: 27-JAN-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1300002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2340  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 468 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-013-895A-2

Query Match 49.4%; Score 1072; DB 4; Length 468;  
Best Local Similarity 54.8%; Pred. NO.1.2e-93;

Matches 234; Conservative 39; Mismatches 114; Indels 40; Gaps 8;

QY 5 GONAPASGARRKRGPGREARGARPGLRVKTIVLVAAVLL-LVSAESALITQODLAP 63  
DB 60 GONHPSAR-ARAGRAPGRPARREASPRLRVHKTFFVYVGLQVPSAATIKLHD--- 115  
QY 64 QORAPQOKRSSPSEGLCPGPHHISEDGRDCISCKYGODYTHNNDLFLCLRTCRDSGE 123  
DB 116 -QSIGTOQWHSPLGELCPGSHRSERPGACNCTEGVGTNASNNLFCACLPCTACKSDE 174  
QY 124 VELSPCTTTRNTVOCCEGTFRREDSPEMCRKCRGTGCGRWVKGDDCTPMSDIECVHES 183  
DB 175 EERSPCTTTRNTVOCCKGTFRNDNSAEMCKKSTGCGRWVKKYKDCIPMSDIECVHES 234  
QY 184 G-----IIGVTVAAVLLVAVFVCKSLMKKVLPLYLGIC---SGGGGDPERVDSS 233  
DB 235 GNGHNIWILVTVPLVLLVAVLI-----VCCIGSGCGGDPKCMDBVC 279  
QY 234 -----ORPAEDNVLNEIYSILO--PTQVPEQEMEYQEPAPRTGVNMLSPGSEHILLE 284  
DB 280 FWRGLGLRGPAEDNAHNEILSNADSLSTFVSEQOMESQEPADLTGVTVOSPGEAOCLLG 339  
QY 285 PAEARSORRLVLPANAGDPTETLRQCFDDFADLVPPDSWEPLMRKLGMDNEIKYAKA 344  
DB 340 PAEAGSORRLVLPANAGDPTETLMLEFDKFAINVPPDSMDQLMRDILTKNEIDVYRA 399  
QY 345 EAAGHRDTLYTMLIKWVKTRGRDASVHTLDLAETLGERLAKOKIEHLLSSGKFMYLEG 404  
DB 400 GTAGPGDALYMLMKWVKTRGRNASHTLTDALERMERHAKKIKQDLVDVSGKFIYED 459  
QY 405 NADSAKS 411  
DB 460 GTGSAYS 466

RESULT 11  
US-09-565-918-2

Sequence 2, Application US/09565918

Patent No. 6433147

GENERAL INFORMATION:

APPLICANT: Ni, Jlan

APPLICANT: Rosen, Craig A.

APPLICANT: Pan, James G.

APPLICANT: Gentz, Reiner L.

APPLICANT: Dixit, Vishva M.  
TITLE OF INVENTION: Death Domain Containing Receptor 4  
FILE REFERENCE: 1488.1300005  
CURRENT APPLICATION NUMBER: US/09/565,918  
CURRENT FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: US 60/132,922  
PRIOR FILING DATE: 1999-05-06  
PRIOR APPLICATION NUMBER: US 09/013,895  
PRIOR FILING DATE: 1998-01-27  
PRIOR APPLICATION NUMBER: US 60/037,829  
PRIOR FILING DATE: 1997-02-05  
PRIOR APPLICATION NUMBER: US 60/035,722  
PRIOR FILING DATE: 1997-01-28  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-565-918-2

Query Match 49.4%; Score 1072; DB 4; Length 468;  
Best Local Similarity 54.8%; Pred. NO.1.2e-93;

Matches 234; Conservative 39; Mismatches 114; Indels 40; Gaps 8;

QY 5 GONAPASGARRKRGPGREARGARPGLRVKTIVLVAAVLL-LVSAESALITQODLAP 63  
DB 60 GONHPSAR-ARAGRAPGRPARREASPRLRVHKTFFVYVGLQVPSAATIKLHD--- 115  
QY 64 QORAPQOKRSSPSEGLCPGPHHISEDGRDCISCKYGODYTHNNDLFLCLRTCRDSGE 123  
DB 116 -QSIGTOQWHSPLGELCPGSHRSERPGACNCTEGVGTNASNNLFCACLPCTACKSDE 174  
QY 124 VELSPCTTTRNTVOCCEGTFRREDSPEMCRKCRGTGCGRWVKGDDCTPMSDIECVHES 183  
DB 175 EERSPCTTTRNTVOCCKGTFRNDNSAEMCKKSTGCGRWVKKYKDCIPMSDIECVHES 234  
QY 184 G-----IIGVTVAAVLLVAVFVCKSLMKKVLPLYLGIC---SGGGGDPERVDSS 233  
DB 235 GNGHNIWILVTVPLVLLVAVLI-----VCCIGSGCGGDPKCMDBVC 279  
QY 234 -----ORPAEDNVLNEIYSILO--PTQVPEQEMEYQEPAPRTGVNMLSPGSEHILLE 284  
DB 280 FWRGLGLRGPAEDNAHNEILSNADSLSTFVSEQOMESQEPADLTGVTVOSPGEAOCLLG 339  
QY 285 PAEARSORRLVLPANAGDPTETLRQCFDDFADLVPPDSWEPLMRKLGMDNEIKYAKA 344  
DB 340 PAEAGSORRLVLPANAGDPTETLMLEFDKFAINVPPDSMDQLMRDILTKNEIDVYRA 399  
QY 345 EAAGHRDTLYTMLIKWVKTRGRDASVHTLDLAETLGERLAKOKIEHLLSSGKFMYLEG 404  
DB 400 GTAGPGDALYMLMKWVKTRGRNASHTLTDALERMERHAKKIKQDLVDVSGKFIYED 459  
QY 405 NADSAKS 411  
DB 460 GTGSAYS 466

RESULT 12

US-09-448-868-2

Sequence 2, Application US/09448868

Patent No. 6461823

GENERAL INFORMATION:

APPLICANT: Ni, Jlan

APPLICANT: Rosen, Craig A.

APPLICANT: Pan, James G.

APPLICANT: Gentz, Reiner L.

APPLICANT: Dixit, Vishva M.

TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death

TITLE OF INVENTION: Receptor 4). Member of the TNF-Receptor

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/448,868  
FILING DATE: HEREMITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/013,895  
FILING DATE: 27-JAN-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: STEEFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488,1300004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 468 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-448-868-2

Query Match 49.4%; Score 1072; DB 4; Length 468;  
Best Local Similarity 54.8%; Pred. No. 1,2e-93;  
Matches 234; Conservative 39; Mismatches 114; Indels 40; Gaps 8;

QY 5 GQNPASGARKRPGPREARPGRLVPTLVVAAVL-LVAESALITQODLAP 63  
DB 60 GQHPSPAR-ARAGRAPGPAPREASPRLRVHKTFKVVGVLLQVVPSSAATIKLHD--- 115  
QY 64 QQRAAPQOKRSSPSEGICPPGHNISEDGRODISCKYGODYSTHNDLFLCLRCTRCSGE 123  
DB 116 -QSTGTQOWEHSPLGELCPGSHRSERPGACNCRCTEGVGTNASNMLFACLPCTACKSDE 174  
QY 124 VELSPCTTTRNTVQCCEGTFREEDSPEMCKRCRTGCPRGWVKVGDCTPMSDIECVHKS 183  
DB 175 EERSPCTTTRNTACQCKPGTFRNDNSAEMCKKSTGCPRGWVKVGDCTPMSDIECVHKS 234  
QY 184 G-----IIGVTVAAVVLVAVFVCKSLMKKVLPLYKIGC-----SGGGDPERVDRSS 233  
DB 235 GNGHNIVVILVTVLVPLVLAVALI-----VCCIGSGCGGDPKCMDBVC 279  
QY 234 -----QRPGEADVINEIYSILO--PTQVPEQEMEVQEPAPBTGVNMLSPGSESHLE 284  
DB 280 FWRGLGRGPAEDNANHEILISNADSLSTFVSEQOMESQEPADLTGTVVOSPGAQCLLG 339  
QY 285 PAEARSQRRRLVPAVNEGDPETTLROCFDFAVLVFPDSEWPLMRKGLMDNEIKYAKA 344  
DB 340 PAEAEQSORRRLVPAVNGADPTETLMLEFDFKFAIVFPDSDQMLRDLTKNEIDVYRA 399  
QY 345 EAACHRTLYTMLIKWVNTKGRDASVHTLLDALETIGERLAKOKIEDHLLSGKFWYLEG 404  
DB 400 GTAGPGDALYAMLKWKVNTKGRNASIHTLLDALEMERERAKKEXIQLDLVDSGKFVYLED 459  
QY 405 NADSAXS 411  
DB 460 GTGSAYS 466

RESULT 13  
US-10-039-785-1

Sequence 1, Application US/10039785  
Patent No. 6538938  
GENERAL INFORMATION:  
APPLICANT: Salcedo et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL  
FILE REFERENCE: PE550  
CURRENT APPLICATION NUMBER: US/10/039,785  
CURRENT FILING DATE: 2002-05-07  
PRIOR APPLICATION NUMBER: 60/369,860  
PRIOR FILING DATE: 2002-04-05  
PRIOR APPLICATION NUMBER: 60/341,237  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 60/331,310  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/331,044  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: 60/327,364  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/323,807  
PRIOR FILING DATE: 2001-09-21  
PRIOR APPLICATION NUMBER: 60/309,176  
PRIOR FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: 60/294,981  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/293,473  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 1  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-039-785-1

Query Match 49.4%; Score 1072; DB 4; Length 468;  
Best Local Similarity 54.8%; Pred. No. 1,2e-93;  
Matches 234; Conservative 39; Mismatches 114; Indels 40; Gaps 8;

QY 5 GQNPASGARKRPGPREARPGRLVPTLVVAAVL-LVAESALITQODLAP 63  
DB 60 GQHPSPAR-ARAGRAPGPAPREASPRLRVHKTFKVVGVLLQVVPSSAATIKLHD--- 115  
QY 64 QQRAAPQOKRSSPSEGICPPGHNISEDGRODISCKYGODYSTHNDLFLCLRCTRCSGE 123  
DB 116 -QSTGTQOWEHSPLGELCPGSHRSERPGACNCRCTEGVGTNASNMLFACLPCTACKSDE 174  
QY 124 VELSPCTTTRNTVQCCEGTFREEDSPEMCKRCRTGCPRGWVKVGDCTPMSDIECVHKS 183  
DB 175 EERSPCTTTRNTACQCKPGTFRNDNSAEMCKKSTGCPRGWVKVGDCTPMSDIECVHKS 234  
QY 184 G-----IIGVTVAAVVLVAVFVCKSLMKKVLPLYKIGC-----SGGGDPERVDRSS 233  
DB 235 GNGHNIVVILVTVLVPLVLAVALI-----VCCIGSGCGGDPKCMDBVC 279  
QY 234 -----QRPGEADVINEIYSILO--PTQVPEQEMEVQEPAPBTGVNMLSPGSESHLE 284  
DB 280 FWRGLGRGPAEDNANHEILISNADSLSTFVSEQOMESQEPADLTGTVVOSPGAQCLLG 339  
QY 285 PAEARSQRRRLVPAVNEGDPETTLROCFDFAVLVFPDSEWPLMRKGLMDNEIKYAKA 344  
DB 340 PAEAEQSORRRLVPAVNGADPTETLMLEFDFKFAIVFPDSDQMLRDLTKNEIDVYRA 399  
QY 345 EAACHRTLYTMLIKWVNTKGRDASVHTLLDALETIGERLAKOKIEDHLLSGKFWYLEG 404  
DB 400 GTAGPGDALYAMLKWKVNTKGRNASIHTLLDALEMERERAKKEXIQLDLVDSGKFVYLED 459  
QY 405 NADSAXS 411  
DB 460 GTGSAYS 466

RESULT 14

US-09-086-483A-6  
Sequence 6, Application US/09086483A  
Patent No. 6214580  
GENERAL INFORMATION:  
APPLICANT: NI, et al.  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/086,483A  
FILING DATE: May-29-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050,936  
FILING DATE: May-30-97  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/069,112  
FILING DATE: Dec-9-97  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PP379  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8439  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-086-483A-6

Query Match 48.9%; Score 1061.5; DB 3; Length 467;  
Best Local Similarity 54.8%; Pred. No. 1.2e-92;  
Matches 234; Conservative 39; Mismatches 113; Indels 41; Gaps 9;

QY 5 GONAPASGARKRRGPGPREARGARPGLRVPKTLVLVVAAYLL-LVSAESALITQODLAP 63  
DB 60 GQHPSPAR-ARAGRAPGRPARREASPRLRVHKTRFVYVGVLLVWPSSAATKLHD-- 115

QY 64 QORAPPOOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNDLLFLCRLCTRCDGE 123  
DB 116 -QSIGTQOWEHSFGLGELCPGSHSRERGCACNCRCTEGVGTMAANNLFCALPCTACKSDE 174

QY 124 VELSPCTTTRNTVQCCEEGTFRREDSPEMCKCKRTGCPRGVAVKGDCTPMSDIECVHES 183  
DB 175 EERSPCTTTRNTACQCKPGTFERNDSAEKCKSTGCPRGVAVKGDCTPMSDIECVHES 234

QY 184 G-----IIIGVTAAYVAVLVAVFVCKSLMKKTLPLKGC-----SGGGDPERVDRSS 233  
DB 235 GNGHNINIVLVTLVLPVLLVAAYLI-----VCCIGSGGGGDPCKMCRVC 279

QY 234 -----QRPGAEDNVINEIVSIQ--PTQVPEOEMEVOEPAEPTGVNMLSPGSEHLL 284  
DB 280 FWRGLGRGAEEDNAINELISNDSLSTFVSEQOMSEQEPADLTGV-VQSPGAQCLLG 338

QY 285 PAEERSQRRRLVLANEGDPTETLRQCFDDFADLVFPDSWEPLMRKLGMDNEIKVAKA 344  
DB 285 PAEERSQRRRLVLANEGDPTETLRQCFDDFADLVFPDSWEPLMRKLGMDNEIKVAKA 344

DB 339 PAEERSQRRRLVLANEGDPTETLMLEFPKFNANIVPEFDSWQDLMRQDLTKNEIDVRA 398  
QY 345 EAAGRPDLTVNLKWKVNGKGRDASVHTLDALETLGERLAKOKIEHLLSSGKFWLLEG 404  
DB 399 GTAGPGDALYAMLKWKVNGKGRNASHTLDALEMERERAKKEXIQLDLVDSGKFITYLED 458

QY 405 NADSAVS 411  
DB 459 GTGSAVS 465

RESULT 15  
US-09-580-212-6  
Sequence 6, Application US/09580212  
Patent No. 6506569  
GENERAL INFORMATION:  
APPLICANT: NI, Jian et al.  
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR10  
FILE REFERENCE: PP379P1  
CURRENT APPLICATION NUMBER: US/09/580,212  
CURRENT FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/136,786  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: 60/142,563  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: 60/144,023  
PRIOR FILING DATE: 1999-07-15  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 6  
LENGTH: 467  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-580-212-6

Query Match 48.9%; Score 1061.5; DB 4; Length 467;  
Best Local Similarity 54.8%; Pred. No. 1.2e-92;  
Matches 234; Conservative 39; Mismatches 113; Indels 41; Gaps 9;

QY 5 GONAPASGARKRRGPGPREARGARPGLRVPKTLVLVVAAYLL-LVSAESALITQODLAP 63  
DB 60 GQHPSPAR-ARAGRAPGRPARREASPRLRVHKTRFVYVGVLLVWPSSAATKLHD-- 115

QY 64 QORAPPOOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNDLLFLCRLCTRCDGE 123  
DB 116 -QSIGTQOWEHSFGLGELCPGSHSRERGCACNCRCTEGVGTMAANNLFCALPCTACKSDE 174

QY 124 VELSPCTTTRNTVQCCEEGTFRREDSPEMCKCKRTGCPRGVAVKGDCTPMSDIECVHES 183  
DB 175 EERSPCTTTRNTACQCKPGTFERNDSAEKCKSTGCPRGVAVKGDCTPMSDIECVHES 234

QY 184 G-----IIIGVTAAYVAVLVAVFVCKSLMKKTLPLKGC-----SGGGDPERVDRSS 233  
DB 235 GNGHNINIVLVTLVLPVLLVAAYLI-----VCCIGSGGGGDPCKMCRVC 279

QY 234 -----QRPGAEDNVINEIVSIQ--PTQVPEOEMEVOEPAEPTGVNMLSPGSEHLL 284  
DB 280 FWRGLGRGAEEDNAINELISNDSLSTFVSEQOMSEQEPADLTGV-VQSPGAQCLLG 338

QY 285 PAEERSQRRRLVLANEGDPTETLRQCFDDFADLVFPDSWEPLMRKLGMDNEIKVAKA 344  
DB 339 PAEERSQRRRLVLANEGDPTETLMLEFPKFNANIVPEFDSWQDLMRQDLTKNEIDVRA 398

QY 345 EAAGRPDLTVNLKWKVNGKGRDASVHTLDALETLGERLAKOKIEHLLSSGKFWLLEG 404  
DB 399 GTAGPGDALYAMLKWKVNGKGRNASHTLDALEMERERAKKEXIQLDLVDSGKFITYLED 458

QY 405 NADSAVS 411  
DB 459 GTGSAVS 465

Search completed: August 4, 2003, 15:21:06

Mon Aug 4 16:29:50 2003

Job time : 31 secs

us-10-052-798-1.ra1



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:19:51 ; Search time 52 Seconds

(without alignments)  
938.659 Million cell updates/sec

Title: US-10-052-798-1

Perfect score: 2169  
Sequence: 1 MEORGONAPASGARRKRG...HLTSGKMYLFGNADSAXS 411

Scoring table: BLUSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published\_Applications\_AA:\*  
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3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppa/PCYUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
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10: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppa/US09C\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2167	99.9	411	9	US-09-757-421-4
3	2167	99.9	411	10	US-09-887-879-11
4	2167	99.9	411	10	US-09-811-088-6
5	2167	99.9	411	10	US-09-892-964-11
6	2167	99.9	411	10	US-10-052-798-1
7	2167	99.9	411	15	US-10-207-655-194
8	2167	99.9	411	15	US-10-314-410-6
9	2163	99.7	411	14	US-10-067-615-2
10	2163	99.7	411	14	US-10-076-754-2
11	2163	99.7	411	14	US-10-076-773-2
12	2160	99.6	411	9	US-09-874-138-2
13	2160	99.6	411	13	US-10-039-785-3
14	2160	99.6	411	13	US-10-005-842-2
15	2152	99.2	411	8	US-08-916-625B-2

16	2133.5	98.4	440	9	US-09-757-421-2
17	2133.5	98.4	440	10	US-09-811-088-4
18	2133.5	98.4	440	15	US-10-314-410-4
19	1610.5	74.3	350	14	US-10-067-615-6
20	1610.5	74.3	350	14	US-10-076-754-6
21	1610.5	74.3	350	14	US-10-076-773-6
22	1597	73.6	303	8	US-08-916-625B-4
23	1072	49.4	468	13	US-10-039-785-1
24	1072	49.4	468	15	US-10-226-296-2
25	1072	49.4	468	15	US-10-226-318-2
26	1072	49.4	468	15	US-10-175-902-2
27	1065	49.1	418	10	US-09-887-879-14
28	1065	49.1	418	10	US-09-992-964-14
29	819.5	37.8	386	13	US-10-039-785-4
30	819.5	37.8	386	15	US-10-066-500-29
31	819.5	37.8	386	15	US-10-028-072-340
32	819.5	37.8	386	15	US-10-121-049-340
33	819.5	37.8	386	15	US-10-123-904-340
34	819.5	37.8	386	15	US-10-140-470-340
35	819.5	37.8	386	15	US-10-175-746-340
36	819.5	37.8	386	15	US-10-176-918-340
37	819.5	37.8	386	15	US-10-176-921-340
38	819.5	37.8	386	15	US-10-002-796-29
39	819.5	37.8	386	15	US-10-066-494-29
40	819.5	37.8	386	15	US-10-066-494-29
41	819.5	37.8	386	15	US-10-137-865-340
42	819.5	37.8	386	15	US-10-140-474-340
43	819.5	37.8	386	15	US-10-142-431-340
44	819.5	37.8	386	15	US-10-143-114-340
45	819.5	37.8	386	15	US-10-140-002-340

## ALIGNMENTS

Sequence 2, Appl1  
Sequence 4, Appl1  
Sequence 4, Appl1  
Sequence 6, Appl1  
Sequence 6, Appl1  
Sequence 6, Appl1  
Sequence 4, Appl1  
Sequence 1, Appl1  
Sequence 2, Appl1  
Sequence 2, Appl1  
Sequence 2, Appl1  
Sequence 14, Appl1  
Sequence 4, Appl1  
Sequence 29, Appl1  
Sequence 340, App  
Sequence 340, App  
Sequence 340, App  
Sequence 340, App  
Sequence 29, Appl1  
Sequence 340, App  
Sequence 340, App  
Sequence 340, App  
Sequence 340, App

RESULT 1  
US-09-828-739-2  
Sequence 2, Application US/09828739  
Patent No. US20020004227A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Chuntarapal, Anan  
TITLE OF INVENTION: Klm, K. Jin  
TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND  
FILE/REFERENCE: P14681 (REVISED)  
CURRENT APPLICATION NUMBER: US/09/828, 739  
CURRENT FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: US 09/329, 633  
PRIOR FILING DATE: 1999-06-10  
PRIOR APPLICATION NUMBER: US 60/089, 253  
PRIOR FILING DATE: 1998-06-12  
NUMBER OF SEQ ID NOS: 2  
SEQ ID NO 2  
LENGTH: 411  
TYPE: PRT  
ORGANISM: human  
FEATURE:  
NAME/KEY: xaa  
LOCATION: 410  
OTHER INFORMATION: xaa - leu or met  
US-09-828-739-2  
Query Match 99.9%; Score 2167; DB 9; Length 411;  
Best local Similarity 100.0%; Pred. No. 8e-187;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEORGONAPASGARRKRGRRARARARPRKTLVVAVALLSAESALITQOD 60  
DB 1 MEORGONAPASGARRKRGRRARARARPRKTLVVAVALLSAESALITQOD 60  
QY LAPQORAPQOKRSPSEGLCPGHHISDQDSCYGGDYTHNNDLFCRCJRCD 120



Db 61 LAPQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGODYSTHWNDLFLCRLCTCD 120  
QY 121 SGEVELSPCTTTRNTVOCCEGTFRREDSPEMCKRCRTGCPRGWVKVGDCTPMSDIECVH 180  
Db 121 SGEVELSPCTTTRNTVOCCEGTFRREDSPEMCKRCRTGCPRGWVKVGDCTPMSDIECVH 180  
QY 181 KESGIIIGVVAAVVLLVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD 240  
Db 181 KESGIIIGVVAAVVLLVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD 240  
QY 241 NVLNEIVSILOPTVPOQEMVOPAPPTGVNMLSPGESEHLLPAPAEERORRLVPA 300  
Db 241 NVLNEIVSILOPTVPOQEMVOPAPPTGVNMLSPGESEHLLPAPAEERORRLVPA 300  
QY 301 NEGDPTELRCCFPDFADLVFPDSMEPLMRKLGIMDEIKVAKAEAGHRDLYTMLIKW 360  
Db 301 NEGDPTELRCCFPDFADLVFPDSMEPLMRKLGIMDEIKVAKAEAGHRDLYTMLIKW 360  
QY 361 VNKTRDASVHTLLDALETLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
Db 361 VNKTRDASVHTLLDALETLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

## RESULT 2

US-09-757-421-4  
Sequence 4, Application US/09757421  
Patent No. US20020048785A1  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas  
TITLE OF INVENTION: NOVEL POLYPEPTIDES WITHIN  
THE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY AND  
USES THEREFOR  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/757,421  
FILING DATE: 10-Jan-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/843,652  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkiohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 09404/026001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 411 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-757-421-4

Query Match 99.9%; Score 2167; DB 9; Length 411;  
Best Local Similarity 99.8%; Pred. No. 8e-187;  
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MEORGONAPASGARKRHGPGPREARGARGLRVPTLVVAAVLLVSAESALITQOD 60

Db 1 MEORGONAPASGARKRHGPGPREARGARGLRVPTLVVAAVLLVSAESALITQOD 60  
QY 61 LAPQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGODYSTHWNDLFLCRLCTCD 120  
Db 61 LAPQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGODYSTHWNDLFLCRLCTCD 120  
QY 121 SGEVELSPCTTTRNTVOCCEGTFRREDSPEMCKRCRTGCPRGWVKVGDCTPMSDIECVH 180  
Db 121 SGEVELSPCTTTRNTVOCCEGTFRREDSPEMCKRCRTGCPRGWVKVGDCTPMSDIECVH 180  
QY 181 KESGIIIGVVAAVVLLVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD 240  
Db 181 KESGIIIGVVAAVVLLVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD 240  
QY 241 NVLNEIVSILOPTVPOQEMVOPAPPTGVNMLSPGESEHLLPAPAEERORRLVPA 300  
Db 241 NVLNEIVSILOPTVPOQEMVOPAPPTGVNMLSPGESEHLLPAPAEERORRLVPA 300  
QY 301 NEGDPTELRCCFPDFADLVFPDSMEPLMRKLGIMDEIKVAKAEAGHRDLYTMLIKW 360  
Db 301 NEGDPTELRCCFPDFADLVFPDSMEPLMRKLGIMDEIKVAKAEAGHRDLYTMLIKW 360  
QY 361 VNKTRDASVHTLLDALETLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
Db 361 VNKTRDASVHTLLDALETLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

## RESULT 3

US-09-887-879-11  
Sequence 11, Application US/09887879  
Patent No. US20020102706A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chantharapai, Anan  
APPLICANT: Gurney, Austin  
APPLICANT: Kim, Kyung Jin  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: APO-2DCR  
FILE REFERENCE: P1110P1  
CURRENT APPLICATION NUMBER: US/09/887,879  
FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: 09/096,500  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: US 60/049,911  
PRIOR FILING DATE: 1997-06-18  
NUMBER OF SEQ ID NOS: 17  
SEQ ID NO 11  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: Unsure  
LOCATION: 410  
OTHER INFORMATION: Xaa may be leucine or methionine  
US-09-887-879-11

Query Match 99.9%; Score 2167; DB 10; Length 411;  
Best Local Similarity 100.0%; Pred. No. 8e-187;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEORGONAPASGARKRHGPGPREARGARGLRVPTLVVAAVLLVSAESALITQOD 60  
Db 1 MEORGONAPASGARKRHGPGPREARGARGLRVPTLVVAAVLLVSAESALITQOD 60  
QY 61 LAPQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGODYSTHWNDLFLCRLCTCD 120  
Db 61 LAPQRAAPQOKRSSPSEGLCPGHHISEDRDCISCKYGODYSTHWNDLFLCRLCTCD 120  
QY 121 SGEVELSPCTTTRNTVOCCEGTFRREDSPEMCKRCRTGCPRGWVKVGDCTPMSDIECVH 180  
Db 121 SGEVELSPCTTTRNTVOCCEGTFRREDSPEMCKRCRTGCPRGWVKVGDCTPMSDIECVH 180

QY 181 KESGIIIGVTVAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGGDDPERVDRSSORPAED 240  
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Db 181 KESGIIIGVTVAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGGDDPERVDRSSORPAED 240  
QY 241 NVLNEIVSIILOPTQVPEQEMEOEPAPPTGVNMLSPGSEHLLLEPAEAERSORRLLYPA 300  
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Db 241 NVLNEIVSIILOPTQVPEQEMEOEPAPPTGVNMLSPGSEHLLLEPAEAERSORRLLYPA 300  
QY 301 NEGDPTETLRQCFDDFADLVLPDPSWEPLMKRLGLMDNEIKVAKAEAGHSDTLTYMLIKV 360  
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Db 301 NEGDPTETLRQCFDDFADLVLPDPSWEPLMKRLGLMDNEIKVAKAEAGHSDTLTYMLIKV 360  
QY 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411  
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Db 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411  
RESULT 4  
US-09-811-088-6  
; Sequence 6, Application US/09811088  
; Patent No. US20020160446A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Gearing, David P.  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGRAMATIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER  
; FILE OF INVENTION: US5  
; FILE REFERENCE: 07334-324001  
; CURRENT APPLICATION NUMBER: US/09/811,088  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: US 09/712,726  
; PRIOR FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: US 08/820,364  
; PRIOR FILING DATE: 1997-03-12  
; PRIOR APPLICATION NUMBER: US 09/757,421  
; PRIOR FILING DATE: 2001-01-10  
; PRIOR APPLICATION NUMBER: US 08/843,652  
; PRIOR FILING DATE: 1997-04-16  
; PRIOR APPLICATION NUMBER: US 08/843,651  
; PRIOR FILING DATE: 1997-04-16  
; PRIOR APPLICATION NUMBER: US 09/354,809  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: US 08/938,365  
; PRIOR FILING DATE: 1997-09-26  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 411  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-09-811-088-6  
Query Match 99.9%; Score 2167; DB 10; Length 411;  
Best Local Similarity 99.8%; Pred. No. 8e-187;  
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 61 LAPOQRAAPQOKRSSPSEGLCPGHNHSEGRDICSCKYGODYSTHNDLLFCLRCTRCD 120  
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QY 181 KESGIIIGVTVAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGGDDPERVDRSSORPAED 240  
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Db 181 KESGIIIGVTVAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGGDDPERVDRSSORPAED 240

QY 241 NVLNEIVSIILOPTQVPEQEMEOEPAPPTGVNMLSPGSEHLLLEPAEAERSORRLLYPA 300  
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Db 301 NEGDPTETLRQCFDDFADLVLPDPSWEPLMKRLGLMDNEIKVAKAEAGHSDTLTYMLIKV 360  
QY 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411  
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Db 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411  
RESULT 5  
US-09-992-964-11  
; Sequence 11, Application US/09992964  
; Patent No. US20020161202A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin  
; APPLICANT: Gueney, Austin  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: Apo-2dcr  
; FILE REFERENCE: P1110  
; CURRENT APPLICATION NUMBER: US/09/992,964  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 08/878,168  
; PRIOR FILING DATE: 1997-06-18  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 11  
; LENGTH: 411  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: 410  
; OTHER INFORMATION: Xaa may be leucine or methionine  
US-09-992-964-11  
Query Match 99.9%; Score 2167; DB 10; Length 411;  
Best Local Similarity 100.0%; Pred. No. 8e-187;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEORGONAPASAGARRKHGPGPREARGARGLRVPKTLVVAVALLLVSAESALITQOD 60  
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Db 1 MEORGONAPASAGARRKHGPGPREARGARGLRVPKTLVVAVALLLVSAESALITQOD 60  
QY 61 LAPOQRAAPQOKRSSPSEGLCPGHNHSEGRDICSCKYGODYSTHNDLLFCLRCTRCD 120  
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Db 61 LAPOQRAAPQOKRSSPSEGLCPGHNHSEGRDICSCKYGODYSTHNDLLFCLRCTRCD 120  
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Db 121 SGEVELSPCTTNTNTVQCCEGTFRREDSPEMCKRCKTGCPRGVAVKVGDCDTPMSDIECVH 180  
QY 181 KESGIIIGVTVAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGGDDPERVDRSSORPAED 240  
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Db 181 KESGIIIGVTVAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGGDDPERVDRSSORPAED 240  
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Db 241 NVLNEIVSIILOPTQVPEQEMEOEPAPPTGVNMLSPGSEHLLLEPAEAERSORRLLYPA 300  
QY 301 NEGDPTETLRQCFDDFADLVLPDPSWEPLMKRLGLMDNEIKVAKAEAGHSDTLTYMLIKV 360  
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Db 301 NEGDPTETLRQCFDDFADLVLPDPSWEPLMKRLGLMDNEIKVAKAEAGHSDTLTYMLIKV 360  
QY 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411  
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Db 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411

RESULT 6  
US-10-052-798-1  
; Sequence 1, Application US/10052798  
; Publication No. US20020150985A1  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camilla W.  
; Ashkenazi, Avi J.  
; Chundharapal, Anan  
; Kim, Kyung J.  
; TITLE OF INVENTION: Apo-2 Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/052,798  
; FILING DATE: 02-No. US20020150985A1-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,029  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1101R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 411 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-052-798-1  
Query Match 99.9%; Score 2167; DB 14; Length 411;  
Best Local Similarity 100.0%; Pred. No. 8e-187;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MEORGNAAPASGARRKHGPGPREARCARPGLRVPKTLVLYVAVALLLVSAESALITQOD 60  
DB 1 MEORGNAAPASGARRKHGPGPREARCARPGLRVPKTLVLYVAVALLLVSAESALITQOD 60  
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DB 61 LAPQORAPPOOKRSPSEGLCPPGHHSSEGRDICSCKYGODYSTHNDLLFCLRCTRCD 120  
QY 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCRKCTGCPRGWVKVGDCTPMSDIECVH 180  
DB 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCRKCTGCPRGWVKVGDCTPMSDIECVH 180  
QY 181 KESGIIIGVYVAVALVAVFVCKSLMKKVLPLYLKGICSGGGGDDPRVDRSSORPGAED 240  
DB 181 KESGIIIGVYVAVALVAVFVCKSLMKKVLPLYLKGICSGGGGDDPRVDRSSORPGAED 240  
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DB 241 NVLNEIYSIILOPVPQEMEVOPAPPTGVNMLSPSESHLLLEPAEARSQRRLLYPA 300  
QY 301 NEGDPTETLRQCFDADFADLVFPDSWEPMLMKRLGLMDNEIKYAKAEAGHRDLYTMLIKW 360  
DB 301 NEGDPTETLRQCFDADFADLVFPDSWEPMLMKRLGLMDNEIKYAKAEAGHRDLYTMLIKW 360

QY 361 VNKTRGDAVHTLLDALETTGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
DB 361 VNKTRGDAVHTLLDALETTGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
RESULT 7  
US-10-207-655-194  
; Sequence 194, Application US/10207655  
; Publication No. US20030118592A1  
; GENERAL INFORMATION:  
; APPLICANT: Ledbetter, Jeffrey A.  
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS  
; FILE REFERENCE: 390069.401C1  
; CURRENT APPLICATION NUMBER: US/10/207,655  
; NUMBER OF SEQ ID NOS: 426  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 194  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-207-655-194  
Query Match 99.9%; Score 2167; DB 15; Length 411;  
Best Local Similarity 99.8%; Pred. No. 8e-187;  
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MEORGNAAPASGARRKHGPGPREARCARPGLRVPKTLVLYVAVALLLVSAESALITQOD 60  
DB 1 MEORGNAAPASGARRKHGPGPREARCARPGLRVPKTLVLYVAVALLLVSAESALITQOD 60  
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DB 61 LAPQORAPPOOKRSPSEGLCPPGHHSSEGRDICSCKYGODYSTHNDLLFCLRCTRCD 120  
QY 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCRKCTGCPRGWVKVGDCTPMSDIECVH 180  
DB 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCRKCTGCPRGWVKVGDCTPMSDIECVH 180  
QY 181 KESGIIIGVYVAVALVAVFVCKSLMKKVLPLYLKGICSGGGGDDPRVDRSSORPGAED 240  
DB 181 KESGIIIGVYVAVALVAVFVCKSLMKKVLPLYLKGICSGGGGDDPRVDRSSORPGAED 240  
QY 241 NVLNEIYSIILOPVPQEMEVOPAPPTGVNMLSPSESHLLLEPAEARSQRRLLYPA 300  
DB 241 NVLNEIYSIILOPVPQEMEVOPAPPTGVNMLSPSESHLLLEPAEARSQRRLLYPA 300  
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DB 301 NEGDPTETLRQCFDADFADLVFPDSWEPMLMKRLGLMDNEIKYAKAEAGHRDLYTMLIKW 360  
QY 361 VNKTRGDAVHTLLDALETTGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
DB 361 VNKTRGDAVHTLLDALETTGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
RESULT 8  
US-10-314-410-6  
; Sequence 6, Application US/10314410  
; Publication No. US20030125540A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Geating, David P.  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER  
; FILE REFERENCE: 07334-324001  
; CURRENT APPLICATION NUMBER: US/10/314,410  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: US/09/811,088  
; PRIOR FILING DATE: 2001-03-16

DR SMART; SM00005; DEATH; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 FT VARIANT 75 75 V -> A.  
 FT VARIANT 89 89 E -> K.  
 FT VARIANT 196 196 E -> K.  
 FT VARIANT 201 201 R -> H.  
 SQ SEQUENCE 333 AA; 37468 MW; 98C17F66762F287 CRC64;

Query Match 9.3%; Score 202; DB 6; Length 333;  
 Best Local Similarity 22.9%; Pred. No. 2.8e-09;

Matches 88; Conservative 59; Mismatches 134; Indels 104; Gaps 16;

QY 34 VPRTLVVAAVLLVSAESALITQODLAPQORAPQOKRSSPSGL-----CP 83  
 DB 8 LPLVITVYVRLSKCVNAQVTDISKGF--ELRKIVTITETQNEGLHGEQFCRNCP 65  
 QY 84 GHH-----ISDGRDCISCKYGGDYSTHMDLFLCLCTRCDSG--EVELSPCTTTRN 134  
 DB 66 GERKARDCTVNEDEPDVPCQEGEYTDKGHFSSKCRCLDCDGHGLEVEIN-CTPTQN 124  
 QY 135 TVCCCEBTEFREDSPEKCRKCRGCGPRGMKVGDCPTWSDIECVHKSGIIGVTVAAV 194  
 DB 125 TKCRCKPNEFNSAVCEHCDPC-TKCKHGII--ECTLTSMTKCKEEDSRSDLPMLCLL 174  
 QY 195 VLIIVAFVCKSLMKKVLPLYLKGICSGGGDPERVDSSORPGAEDNVLEIVSITLPTQ 254  
 DB 175 -----LWICLLILLLLLPRIYVVIK-----EPCRRKRENGPHSTLTN----- 215  
 QY 255 VPQEMEVOEPAEPTGVNMLSPGSEHLLPEAEERSQRRLLVPANEGDPTETLRQCFD 314  
 DB 216 -PE-----TAINLSDVLSKYITTTAGA-----MTLSQVKD 245  
 QY 315 DFADLVPPDSMEPLMRKIGLMDNEIKVAKAAGHROT---YMLIKVWKKTGDSVH 371  
 DB 246 -----FVRKNGV--SEAKIDEIKNDVQDAEQVOLLRMWYOLHGKQACD 290  
 QY 372 TLDALE-----TLGERLAKOKIED 391  
 DB 291 TLINGLKTADLCTLAEKIHAVILKD 315

## RESULT 9

Q9BDN0 PRELIMINARY; PRT: 331 AA.  
 AC Q9BDN0.  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE FAS antigen CD95.  
 OS Macaca nemestrina (Pig-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Macaca.  
 OX NCBI\_TaxID=9545;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21383618; PubMed=11491535;  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansati A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 RT Fas/Fas-ligand and co-stimulatory molecules.";  
 RT Immunogenetics 53:315-328(2001).  
 RL EMBL; AF344850; AAK37610.1; -.  
 DR EMBL; AF344850; AAK37610.1; -.  
 DR HSSP; P25445; 1DDF.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 2.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.

DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 SQ SEQUENCE 331 AA; 37254 MW; ACFE3DA12C94765 CRC64;

Query Match 9.1%; Score 197; DB 6; Length 331;  
 Best Local Similarity 22.9%; Pred. No. 7.5e-09;

Matches 88; Conservative 56; Mismatches 135; Indels 106; Gaps 16;

QY 34 VPRTLVVAAVLLVSAESALITQODLAPQORAPQOKRSSPSGL-----CP 83  
 DB 8 LPLVITVYVRLSKCVNAQVTDISKGF--ELRKIVTITETQNEGLHGEQFCRNCP 65  
 QY 84 GHH-----ISDGRDCISCKYGGDYSTHMDLFLCLCTRCDSG--EVELSPCTTTRN 134  
 DB 66 GERKARDCTVNEDEPDVPCQEGEYTDKGHFSSKCRCLDCDGHGLEVEIN-CTPTQN 124  
 QY 135 TVCCCEBTEFREDSPEKCRKCRGCGPRGMKVGDCPTWSDIECVHKSGIIGVTVAAV 194  
 DB 125 TKCRCKPNEFNSAVCEHCDPC-TKCKHGII--ECTLTSMTKCKEEDSRSDLPMLCLL 181  
 QY 195 VLIIVAFVCKSLMKKVLPLYLKGICSGGGDPERVDSSORPGAEDNVLEIVSITLPTQ 254  
 DB 182 LLIPPI-----YVVIKAC-----RKHKRENGPHSTLTN----- 213  
 QY 255 VPQEMEVOEPAEPTGVNMLSPGSEHLLPEAEERSQRRLLVPANEGDPTETLRQCFD 314  
 DB 214 -PE-----TAINLSDVLSKYITTTAGA-----MTLSQVKD 243  
 QY 315 DFADLVPPDSMEPLMRKIGLMDNEIKVAKAAGHROT---YMLIKVWKKTGDSVH 371  
 DB 244 -----FVRKNGV--SEAKIDEIKNDVQDAEQVOLLRMWYOLHGKQACD 288  
 QY 372 TLDALE-----TLGERLAKOKIED 391  
 DB 289 TLINGLKTADLCTLAEKIHAVILKD 313

## RESULT 10

Q9TSN4 PRELIMINARY; PRT: 331 AA.  
 AC Q9TSN4.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Death receptor Fas (Apo-1/CD95).  
 GN FAS.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20237686; PubMed=10773350;  
 RA Murayama Y., Terao K., Inoue-Murayama M.;  
 RT "Molecular cloning and characterization of cynomolgus monkey Fas.";  
 RT Hum. Immunol. 61:474-485(2000).  
 RL EMBL; AB031420; BAA83551.1; -.  
 DR HSSP; P25445; 1DDF.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 2.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor.  
 SQ SEQUENCE 331 AA; 37265 MW; 0C617508081B05DF CRC64;

Query Match 9.0%; Score 196; DB 6; Length 331;  
 Best Local Similarity 22.9%; Pred. No. 9.2e-09;  
 Matches 88; Conservative 56; Mismatches 135; Indels 106; Gaps 16;

```

OY 34 VPKTUVAALVAAVLIVSVESALITOODLAPPOORAPAOQRSSPSEU-----CP 83
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 LPVLIVSVRRLLSKCVMAOYDIISSKG--ELRKVITTIETONLBEGLHHEGCFRNP 65
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 84 GHH-----ISEDGDCISCKYGOYDSTHWMDLFLCRLCTRCDSG--EVELSPCTT 134
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 GERKARDCTVNEDEPDVCPOEGKEXYTDKGHPSKRCRLDEGHGLEVEIN-CTR 124
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 135 TVCOEEBGTFRFEDBSPENCRCRKTGCPKRMVVGDCTPMSDIECVHKEGIIIGTVAAV 194
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 TKCRCKPNEFCNSAVCEHGDPC--TKCEHIIIE--ECTLLSNPKCEKDEDSRDL 181
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 195 VLIIVAVFCKSLMKKVLPLYLKIGISGGGGDEPRVDRSSQRBGAENNVLEIYSILQ 254
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 LLIPPI-----VYVVIKAC-----KKHKNQOGHHESTLTN----- 213
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 255 VPDEMEVOEPAEPTGVNMLSPGESEHLEPAEAERSORRLLVPANEGDPTETLRQCPD 314
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 214 -PE-----TAINLSVDVLSKYITTTIGA-----MTLSQVND 243
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 315 DFADLVPRDSWEPLMRKLLGMDNETIKVAKAEAGHBDLT--YTMILKVNKTRGDASV 371
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 244 -----FVRKNGV--SEAKIDEIKNDVNODTAEQKVOLLRNMYQLHGKKDADC 288
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 372 TLLOALE-----TLGERLAKOKIED 391
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 TLIRGLKTADICTLAEKITHAVILKD 313
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 11	
Q9BDN4	
ID Q9BDN4	PRELIMINARY;
NC Q9BDN4	PRT; 331 AA

DT	01-JUN-2001	(TREMBLrel. 17, created)
DT	01-JUN-2001	(TREMBLrel. 17, last sequence update)
DT	01-MAR-2003	(TREMBLrel. 23, last annotation update)
DE	FAS antigen CD95.	
OS	Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).	
OC	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;	
OC	Cercopitheciinae; Cercopithecus.	
OX	NCBI_TaxID:9531;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE-21383618; PubMed-11491535;	
RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,	
RA	Weiss W.R., Ansari A.A.;	
RT	"Cloning, sequencing, and homology analysis of nonhuman primate	
RL	Fas/FasL ligand and co-stimulatory molecules.";	
SL	Immunogenetics 53:315-328(2001).	
DR	EMBL; AF344843; AK37602.1; -.	
DR	HSSP; P23445; IDPF.	
DR	InterPro; IPR000488; Death.	
DR	InterPro; IPR001368; TNFR_c6.	
DR	Pfam; PF000531; death.1.	
DR	Pfam; PF000020; TNFR_c6; 2.	
DR	SMART; SM00005; DEATH; 1.	
DR	SMART; SM00208; TNFR; 2.	
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.	
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.	
FT	VARIANT	44 44 I -> V.
FT	VARIANT	47 47 R -> Q.
FT	VARIANT	55 55 R -> D.
FT	VARIANT	60 60 R -> H.
FT	VARIANT	61 61 N -> S.
FT	VARIANT	77 77 E -> G.
FT	VARIANT	95 95 G -> A.
FT	VARIANT	282 282 E -> G.
FT	VARIANT	298 298 G -> D.
FT	VARIANT	300 300 C -> *.
SO	SEQUENCE	331 AA; 37277 MW; IDB843C4DEID343F4 CRC64;

[illegible]

RESULT 12	
Q9GL40	
ID Q9GH40	PRELIMINARY;
1 090710	PRT; 334 AA

```

DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Fas antigen.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A..
RA      Shui B., Chi L., Zhang Y.R.;
RT      "Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";
RL      Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
RL      EMBL: AY007572; AAC16762.1; -.
DR      HSSP; P25445; 1DDF.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR001368; TNFR_c6.
DR      Pfam; PF000020; TNFR_c6; 2.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00208; TNFR; 2.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
DR      PROSITE; PS00652; TNFR_NGFR_1; 2.
DR      PROSITE; PS00500; TNFR_NGFR_2; 2.
SQ      SEQUENCE 334 AA; 37531 MW; 2DC5B161C3191C6 CRC64;

```

Query Match	Score	DB	Length
9.08;	194.5;	DB 6;	334;

Best Local Similarity 23.68; Pred. No. 1.3e-08;

Matches 92; Conservative 58; Mismatches 123; Indels 117; Gaps 20;

[illegible]

```
38 LVLVAAVLLVSAESALITQ-QDLAP--QQRAPQQRSSPSEGL-----C 83
```

[illegible]

8 LPLVLTSVRLLS--KCVIAQVTDISSKGFELRKIVTTIETQNLEGLHHEGQFCRNPCPP 65

```
Y      84 GHH-----ISEGDCISCKYGQDYSTHWNDLFLCLRCTRCDSG---EVELSPCTTTRN 134
```

[illegible]



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OY      130  TTRNTVQCEGGTFR-----DSDPMCKRCR-----157
Db      115  SAKSDTHCCGCGSMWCDSITVPCGASSPFCVPCGATTPVHNEPTRPCLPRTYINGNDC 174
OY      158  TGCPRGMKV--GDCTP--MSDIECVKESGIIIGTVAAVLVIAVFCSLMKKYL 212
Db      175  TSCPGRGSSVCPKATAVCGMKOMFWY---VLLGV---AFLEFALILCAICRMOPC 226
OY      213  PYLKGICGGG--GDPERVDRSSQ-----RPAEDVNLNETVSILOTPQV--RCQEME 261
Db      227  AVVTDATGTERLASPQTHLASPSAHITLMPSTGKICTYVOLGNWNPFGLSQTOE 286
OY      262  V-----QEPADPCVNMILSGESENHLEPRAVLEKSQRRRLVPRANEDPTETLR 310
Db      287  VVCGASQPMDDLPNRTLSTPLASP---LSPAP-----PA--GSPAAYLQ 327
OY      311  --QCPDDEADLVLPFSPWEPLMKRLGIMDNEIKVAKAEAGHRDLYTLMIKWNKTCGRDA 368
Db      328  GPOLY-DVMDAVPARMKKEFVTLTGREAETEAVEIETCRFDQOYEMLKRW--RQOQPA 384
OY      369  SVNHTLDALETIG 381
Db      385  GIGATYAADLKKRG 397

```

RESULT	15			
09GK28		PRELIMINARY;	PRT;	310 AA.
09GK28				
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2001 (TrEMBLrel. 16, last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, last annotation update)			
DE	Fas antigen Apo-1/CD95.			
GN	FAS.			
OS	Macaca acetoidea (Stump-tailed macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_TaxID=9540;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Chl L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;			
RT	"Cloning of fas gene in stump-tailed monkey.";			
RL	Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF32357; AAG4394.1; -			
DR	HSSP; P25445; 1DDF.			
DR	InterPro; IPR000488; Death.			
DR	InterPro; IPR001368; TNFR_c6.			
DR	Pfam; PF00551; death_1.			
DR	Pfam; PF00020; TNFR_c6; 2.			
DR	SMART; SM00005; DEATH_1.			
DR	SMART; SM00208; TNFR; 2.			
DR	PROSITE; PSS0017; DEATH_DOMAIN; 1.			
DR	PROSITE; PSS0050; TNFR_NGFR_2; 2.			
SO	SEQUENCE 310 AA: 34806 MW; C5C799F1E804A419 CRC64;			

Query Match	8.7%	Score 188.5;	DB 6;	Length 310;
Best Local Similarity	22.9%	Pred. No. 3.8e-08;		
Matches	88;	Conservative	50;	Mismatches 120;
			Indels	127;
			Gaps	17;

[illegible]

```

OY      195  VLIIVAVVCSSLLMKKLYLEPKLKGICSGGGGDEDERIDRSSRGADNYIVLSLPQ  254
          ||      ||      ||      ||      ||      ||      ||      ||
Db      172  -----KK-----PCKRHKRENGCPHSTLTN-----192

OY      255  VPDEQMEVQRAPEPTGVNMLSPGESEHLLPEAERSSORRLLYPANEGDPTETLRQCFD  314
          ||      ||      ||      ||      ||      ||      ||      ||
Db      193  -PE-----TAINLSDVDLSIKYTTIGA-----MTLSQVKD  222

OY      315  DFADLVFDSNEPLMKRLGLMDNEIKVAKAEAGHROL--YTMILKKNVAKTGRDASVH  371
          ||      ||      ||      ||      ||      ||      ||      ||
Db      223  -----FVRKNGV--SEAKTDEIKNNHVODTAEQKVOLLRNMYQLHKKKACD  267

OY      372  TLIDALE-----TLGRLAKOKIED  391
          ||      ||      ||      ||      ||      ||      ||      ||
Db      268  TLIKGLKTADLCYLAERKIHAVILKD  292

```

Search completed: August 4, 2003, 15:19:42  
Job time : 101 secs

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OY 195 VLIIVAVVCKSLIMKKVLEPYLKIGICSGGGGDEPVRVDRSSQRPAGADNVINEIVSILQPTQ 254
Db 172 -----KK-----PCKHKRENQCPHTESTLN----- 192
OY 255 VPEOEMEVOEPAEPYGVNMLSPGESEHLLPEPAEAERSQRRLLVPANEGDPTETLRQCFD 314
Db 193 -PE-----TAINLSVDVLSKXYTTIAGA-----MTLSQVKD 222
OY 315 DFADLVPFDSMEPLMKRLGLMDNETKVAKAEAGHRDTL---YTMLIKVVNKTGRDASVH 371
Db 223 -----FVRKNGV--SEAKIDEIKNNHNVODTAEQKVOLLRNWYQLHGKKDQACD 267
OY 372 TLLDALE----TJGERLAKOKIED 391
Db 268 TLIKGLKTADLCTLAERKIHAVILKD 292

Search completed: August 4, 2003, 15:19:42
Job time : 101 secs

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OY 241 NVLNEIVSILOPTQVPEQEMEVOEPAEPTGVNMLSPGESEHLLLEPAEERSORRLLVPA 300
DB 241 NVLNEIVSILOPTQVPEQEMEVOEPAEPTGVNMLSPGESEHLLLEPAEERSORRLLVPA 300
OY 301 NEGDPTELRQCFDFADLVFPDSMEPLMRKLGIMDNIEIKYAKAEAGHRTLYTMLIKW 360
DB 301 NEGDPTELRQCFDFADLVFPDSMEPLMRKLGIMDNIEIKYAKAEAGHRTLYTMLIKW 360
OY 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
```

## RESULT 11

```
US-10-076-773-2
: Sequence 2, Application US/10076773
: Publication No. US20020161196A1
: GENERAL INFORMATION:
: APPLICANT: Alnemrl, Enad S.
: TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
: FILE REFERENCE: 480140.432D2
: CURRENT APPLICATION NUMBER: US/10/076,773
: CURRENT FILING DATE: 2002-02-12
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 2
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-076-773-2
```

```
Query Match 99.7%; Score 2163; DB 14; Length 411;
Best Local Similarity 99.5%; Pred. No. 1.8e-186;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MEORGONAPPAASGARKRHGPGPREARGARPLRVKTLVLYAAVLLVSAESALITQOD 60
DB 1 MEORGONAPPAASGARKRHGPGPREARGARPLRVKTLVLYAAVLLVSAESALITQOD 60
OY 61 LAPORAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNMNLLFCLRCTCD 120
DB 61 LAPORAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNMNLLFCLRCTCD 120
OY 121 SGEVELSPCTTNTNTVQCEGTFREEDSPMKCRKCTGCGPRGKVKGDCDTPMSDIECVH 180
DB 121 SGEVELSPCTTNTNTVQCEGTFREEDSPMKCRKCTGCGPRGKVKGDCDTPMSDIECVH 180
OY 181 KESGIIIGVYAAVLLVAVFVCKSLMKKVLPLYLKIGCSGGGDDPERVDRSSORPGAED 240
DB 181 KESGIIIGVYAAVLLVAVFVCKSLMKKVLPLYLKIGCSGGGDDPERVDRSSORPGAED 240
OY 241 NVLNEIVSILOPTQVPEQEMEVOEPAEPTGVNMLSPGESEHLLLEPAEERSORRLLVPA 300
DB 241 NVLNEIVSILOPTQVPEQEMEVOEPAEPTGVNMLSPGESEHLLLEPAEERSORRLLVPA 300
OY 301 NEGDPTELRQCFDFADLVFPDSMEPLMRKLGIMDNIEIKYAKAEAGHRTLYTMLIKW 360
DB 301 NEGDPTELRQCFDFADLVFPDSMEPLMRKLGIMDNIEIKYAKAEAGHRTLYTMLIKW 360
OY 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
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## RESULT 12

```
US-09-874-138-2
: Sequence 2, Application US/09874138
: Patent No. US20020072091A1
: GENERAL INFORMATION:
: APPLICANT: Ni, Jian
: APPLICANT: Gentz, Reiner L.
: APPLICANT: Yu, Guo-liang
```

```
: APPLICANT: Rosen, Craig A.
: TITLE OF INVENTION: Death Domain Containing Receptor 5
: FILE REFERENCE: 1488.1310006
: CURRENT APPLICATION NUMBER: US/09/874,138
: CURRENT FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 09/565,009
: PRIOR FILING DATE: 2000-05-04
: PRIOR APPLICATION NUMBER: 60/148,939
: PRIOR FILING DATE: 1999-08-13
: PRIOR APPLICATION NUMBER: 60/133,238
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/132,498
: PRIOR FILING DATE: 1999-05-04
: PRIOR APPLICATION NUMBER: 09/042,583
: PRIOR FILING DATE: 1998-03-17
: PRIOR APPLICATION NUMBER: 60/054,021
: PRIOR FILING DATE: 1997-07-29
: PRIOR APPLICATION NUMBER: 60/040,846
: PRIOR FILING DATE: 1997-03-17
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 2
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-874-138-2
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Query Match 99.6%; Score 2160; DB 9; Length 411;
Best Local Similarity 99.5%; Pred. No. 3.4e-186;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MEORGONAPPAASGARKRHGPGPREARGARPLRVKTLVLYAAVLLVSAESALITQOD 60
DB 1 MEORGONAPPAASGARKRHGPGPREARGARPLRVKTLVLYAAVLLVSAESALITQOD 60
OY 61 LAPORAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNMNLLFCLRCTCD 120
DB 61 LAPORAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNMNLLFCLRCTCD 120
OY 121 SGEVELSPCTTNTNTVQCEGTFREEDSPMKCRKCTGCGPRGKVKGDCDTPMSDIECVH 180
DB 121 SGEVELSPCTTNTNTVQCEGTFREEDSPMKCRKCTGCGPRGKVKGDCDTPMSDIECVH 180
OY 181 KESGIIIGVYAAVLLVAVFVCKSLMKKVLPLYLKIGCSGGGDDPERVDRSSORPGAED 240
DB 181 KESGIIIGVYAAVLLVAVFVCKSLMKKVLPLYLKIGCSGGGDDPERVDRSSORPGAED 240
OY 241 NVLNEIVSILOPTQVPEQEMEVOEPAEPTGVNMLSPGESEHLLLEPAEERSORRLLVPA 300
DB 241 NVLNEIVSILOPTQVPEQEMEVOEPAEPTGVNMLSPGESEHLLLEPAEERSORRLLVPA 300
OY 301 NEGDPTELRQCFDFADLVFPDSMEPLMRKLGIMDNIEIKYAKAEAGHRTLYTMLIKW 360
DB 301 NEGDPTELRQCFDFADLVFPDSMEPLMRKLGIMDNIEIKYAKAEAGHRTLYTMLIKW 360
OY 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
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## RESULT 13

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US-10-039-785-3
: Sequence 3, Application US/10039785
: Publication No. US20020067646A1
: GENERAL INFORMATION:
: APPLICANT: Salcedo et al.
: TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL
: FILE REFERENCE: PR550
: CURRENT APPLICATION NUMBER: US/10/039,785
: CURRENT FILING DATE: 2002-05-07
: PRIOR APPLICATION NUMBER: 60/369,860
: PRIOR FILING DATE: 2002-04-05
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PRIOR APPLICATION NUMBER: 60/341,237  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 60/331,310  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/331,044  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: 60/327,364  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/323,807  
PRIOR FILING DATE: 2001-09-21  
PRIOR APPLICATION NUMBER: 60/309,176  
PRIOR FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: 60/294,981  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/293,473  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 3  
LENGTH: 411  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-039-785-3

Query Match 99.6%; Score 2160; DB 13; Length 411;  
Best Local Similarity 99.5%; Pred. No. 3,4e-186;  
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEORGNAPASAGARRHGGPREARGARGLVPTLVVAVALVLSAESALLTQOD 60  
DB 1 MEORGNAPASAGARRHGGPREARGARGLVPTLVVAVALVLSAESALLTQOD 60  
QY 61 LAPQORAPPOOKRSSSEGLCPRGHHISEDRDCISCKYGQDYSTMNDLLFCLRCTCD 120  
DB 61 LAPQORAPPOOKRSSSEGLCPRGHHISEDRDCISCKYGQDYSTMNDLLFCLRCTCD 120  
QY 121 SGEVELSPCTTNTNTVCOCEEGTFREEDSPEMCRKCTGCPRGVAVGDCPTPMSDIECVH 180  
DB 121 SGEVELSPCTTNTNTVCOCEEGTFREEDSPEMCRKCTGCPRGVAVGDCPTPMSDIECVH 180  
QY 181 KESGIIIGTVAAVVLIVAFVCKSLMKKVLPLYLKGICSGGGGDPERVDROSSORGAED 240  
DB 181 KESGIIIGTVAAVVLIVAFVCKSLMKKVLPLYLKGICSGGGGDPERVDROSSORGAED 240  
QY 241 NVLNEIVSILQPVPEQEMEVOEPAEPTGVNMLSPGSESHLLPEAEERSQRRLLVPA 300  
DB 241 NVLNEIVSILQPVPEQEMEVOEPAEPTGVNMLSPGSESHLLPEAEERSQRRLLVPA 300  
QY 301 NEGDPTETLRQCFDDADLVPPDSWEPMLMKKLGMLMNEIKVAKAEAGHRTLYTMLIKW 360  
DB 301 NEGDPTETLRQCFDDADLVPPDSWEPMLMKKLGMLMNEIKVAKAEAGHRTLYTMLIKW 360  
QY 361 VNKTRDASVHTLLDLALETIGERLAKOKIEDHLLSSGKFMYLEGNDASAXS 411  
DB 361 VNKTRDASVHTLLDLALETIGERLAKOKIEDHLLSSGKFMYLEGNDASAXS 411

RESULT 14  
US-10-005-842-2  
Sequence 2, Application US/10005842  
Publication No. US20020098550A1  
GENERAL INFORMATION:  
APPLICANT: NI, Jian  
Gentz, Reiner  
Yu, Guo-Liang  
Su, Jeffrey  
Rosen, Craig A.  
TITLE OF INVENTION: Death Domain Containing Receptor 5  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville

STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/005,842  
FILING DATE: 07-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,583  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 60/040,846  
FILING DATE: 17-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hoover, Kenley  
REGISTRATION NUMBER: 40,302  
REFERENCE/DOCKET NUMBER: PP366  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 3013098504  
TELEFAX: 3013098439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 411 amino acids  
TYPE: amino acid  
MOLECULE TYPE: protein  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-005-842-2

Query Match 99.6%; Score 2160; DB 13; Length 411;  
Best Local Similarity 99.5%; Pred. No. 3,4e-186;  
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEORGNAPASAGARRHGGPREARGARGLVPTLVVAVALVLSAESALLTQOD 60  
DB 1 MEORGNAPASAGARRHGGPREARGARGLVPTLVVAVALVLSAESALLTQOD 60  
QY 61 LAPQORAPPOOKRSSSEGLCPRGHHISEDRDCISCKYGQDYSTMNDLLFCLRCTCD 120  
DB 61 LAPQORAPPOOKRSSSEGLCPRGHHISEDRDCISCKYGQDYSTMNDLLFCLRCTCD 120  
QY 121 SGEVELSPCTTNTNTVCOCEEGTFREEDSPEMCRKCTGCPRGVAVGDCPTPMSDIECVH 180  
DB 121 SGEVELSPCTTNTNTVCOCEEGTFREEDSPEMCRKCTGCPRGVAVGDCPTPMSDIECVH 180  
QY 181 KESGIIIGTVAAVVLIVAFVCKSLMKKVLPLYLKGICSGGGGDPERVDROSSORGAED 240  
DB 181 KESGIIIGTVAAVVLIVAFVCKSLMKKVLPLYLKGICSGGGGDPERVDROSSORGAED 240  
QY 241 NVLNEIVSILQPVPEQEMEVOEPAEPTGVNMLSPGSESHLLPEAEERSQRRLLVPA 300  
DB 241 NVLNEIVSILQPVPEQEMEVOEPAEPTGVNMLSPGSESHLLPEAEERSQRRLLVPA 300  
QY 301 NEGDPTETLRQCFDDADLVPPDSWEPMLMKKLGMLMNEIKVAKAEAGHRTLYTMLIKW 360  
DB 301 NEGDPTETLRQCFDDADLVPPDSWEPMLMKKLGMLMNEIKVAKAEAGHRTLYTMLIKW 360  
QY 361 VNKTRDASVHTLLDLALETIGERLAKOKIEDHLLSSGKFMYLEGNDASAXS 411  
DB 361 VNKTRDASVHTLLDLALETIGERLAKOKIEDHLLSSGKFMYLEGNDASAXS 411

RESULT 15  
US-08-916-625B-2  
Sequence 2, Application US/08916625B  
Publication No. US20010010924A1  
GENERAL INFORMATION:  
APPLICANT: DEEN, KEITH C.  
YOUNG, PETER R.

Search completed: August 4, 2003, 15:28:55  
 Job time : 54 secs

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: TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
: TITLE OF INVENTION: RECEPTOR, TR6
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: RATNER & PRESTIA
: STREET: P.O. BOX 980
: CITY: VALLEY FORGE
: STATE: PA
: COUNTRY: USA
: ZIP: 19482
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/916,625B
: FILING DATE: 22-AUG-1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/853,684
: FILING DATE: 09-MAY-1997
: APPLICATION NUMBER: 60/041,230
: FILING DATE: 14-MARCH-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: PRESTIA, PAUL F
: REGISTRATION NUMBER: 23,031
: REFERENCE/DOCKET NUMBER: GH-50008-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-407-0700
: TELEFAX: 610-407-0701
: TELEX: 846169
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 411 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-916-625B-2
    
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Query Match 99.28; Score 2152; DB 8; Length 411;  
 Best Local Similarity 99.3%; Pred. No. 1.8e-185;  
 Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MEORGONAPASGARRKRGPPRGARGRLVYKTLVVAVALLLVSAESALITQOD 60
Db 1 MEORGONAPASGARRKRGPPRGARGRLVYKTLVVAVALLLVSAESALITQOD 60
QY 61 LAPQORAAPOOKRSSPSEGLCPGHNISEDGRDCISCKYGODYSTHNDLLFCLCTRC 120
Db 61 LAPQORAAPOOKRSSPSEGLCPGHNISEDGRDCISCKYGODYSTHNDLLFCLCTRC 120
QY 121 SGEVEISPTCTTNTNTVCQCEBGTFRREDSPEMCKRCKTGCPRGWVKVGDCTPMSDIECVH 180
Db 121 SGEVEISPTCTTNTNTVCQCEBGTFRREDSPEMCKRCKTGCPRGWVKVGDCTPMSDIECVH 180
QY 121 SGEVEISPTCTTNTNTVCQCEBGTFRREDSPEMCKRCKTGCPRGWVKVGDCTPMSDIECVH 180
Db 121 SGEVEISPTCTTNTNTVCQCEBGTFRREDSPEMCKRCKTGCPRGWVKVGDCTPMSDIECVH 180
QY 181 KESGIIIGTVAVALVAVVAVVCKSLMKKVLPLKIGICSGGGDPERVDRSSORPGAED 240
Db 181 KESGIIIGTVAVALVAVVAVVCKSLMKKVLPLKIGICSGGGDPERVDRSSORPGAED 240
QY 241 NVLNEIYSIIQPTQVPEQEMEVOEPAPETGVNMLSPGSEHLLLEPAEERSORRLVPA 300
Db 241 NVLNEIYSIIQPTQVPEQEMEVOEPAPETGVNMLSPGSEHLLLEPAEERSORRLVPA 300
QY 301 NESDPTETLRQCFDDFADLVFPDSWEPLMKRLGIMDNEIKVAKAEAGHRDTLYTMLIKW 360
Db 301 NESDPTETLRQCFDDFADLVFPDSWEPLMKRLGIMDNEIKVAKAEAGHRDTLYTMLIKW 360
QY 361 VNTGGRASVHTLLDAETLGERLAKOKIDHLLSSGKEMYLEGNADSAXS 411
Db 361 VNTGGRASVHTLLDAETLGERLAKOKIDHLLSSGKEMYLEGNADSAXS 411
    
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Db 122 NGSEFLPDQACEVCKK-SRCKEDEFETKSCTAISNVCKRNSGSGSTSTFTYIMPLI 180  
 OY 199 AVEVCKSKSL--WKVLYPLKIGICSGG-----GDPERYDRSSQRPAGEEDNVINEIVS 248  
 Db 181 VLLACVLCIYWTWSKONKTAVTSPREMKIKGDESEVREEQN---DHSNRIDDS 237  
 OY 249 ILQPTQVPEDEMEVOEPAEPTGVNMLSPGESEHLLPEAERSQRRLVPAVEDPDET 308  
 Db 238 QLR-----FILEQVVESSSRRLVPSGE---ES 264  
 OY 309 LROCFDEPDADLVPPDSWPLMKRLGLMDNEIKVAEAGHDTLYMLIKVNTGGRN 368  
 Db 265 LKRTDFDEEE-IDVHYHNRFFRLIGLSDNAIK--SAESLFFEDRVYELKLTWMEKEGLKA 321  
 OY 369 SVHTLLDALFTIGERLAKOKIEDHLLSGKFWYLE 403  
 Db 322 DFNSLIDALYLDORLSAENIIAKAINNSCFKYE 356

## RESULT 6

O9BY82 PRELIMINARY: PRT: 48 AA.  
 AC O9BY82:  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE Death receptor 5 (Fragment).  
 GN DR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yoshida T., Maeda A., Tani N., Sakai T.;  
 RT "Promoter structure and transcription initiation sites of the human  
 death receptor 5 gene."  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB054004; BAB39708.1;  
 KW Receptor.  
 FT NON\_TER  
 SQ SEQUENCE 48 AA: 5008 MW: E90E27D81A5EF30A CRC64;

Query Match 10.7%; Score 233; DB 4; Length 48;  
 Best Local Similarity 97.9%; Pred. No. 4.3e-13;  
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MEORGQNPASGARRHGPPREARGARPGLEVPKTLVLYVAAYLL 48  
 Db 1 MEORGQNPASGARRHGPPREARGARPGLEVPKTLVLYVAAYLL 48

## RESULT 7

O8VD70 PRELIMINARY: PRT: 387 AA.  
 AC O8VD70:  
 DT 01-MAR-2002 (Tremblrel. 20, Created)  
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Similar to tumor necrosis factor receptor superfamily, member 12.  
 DE TNFRSF25 OR TNFRSF12.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Straussberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC017526; AAH1756.1;  
 DR MGD; MGI:193467; Tnfk125.  
 DR InterPro; IPR000488; Lach.

DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 2.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 2.  
 DR PROSITE; PSS0017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_2; 1.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 387 AA: 41640 MW: F1664466BAD68D3 CRC64;

Query Match 9.5%; Score 206; DB 11; Length 387;  
 Best Local Similarity 24.7%; Pred. No. 1.5e-09;  
 Matches 101; Conservative 46; Mismatches 176; Indels 86; Gaps 23;

OY 15 RKRHGRPREARARG--LRVPKTLVLYVAAYLLV---SASALITOODLAPQORAP 69  
 Db 7 RERSPPG-----AATGSTARVQLPLFLPLLLLLLGQGGGSGRCDASE----- 56  
 OY 70 QOKRSP--SEGICPPGHHISE-----DGRDCISGKGODYSTHNDL-LFCLRCTCD 120  
 Db 57 SQRRGPPCCRG-CPKGHYKAPCAEPCGSGTCLPCD-SPTFLTRDNHFTDCTRCQYCD 114  
 OY 121 SG--EVELSPCTTTRNTYQCEGTEREDSPMCRCRTGCPRGMYKVGDCIPTSDDIC 178  
 Db 115 EELQVYTLKNSAKSSTHGCQSG-----WCYDCSRE-PCGKSSPSVCYPCGATTP 164  
 OY 179 VHKESGIT--IGTVAAVLYVAAYVYCKSLMKKVLPLKIGICSGG--GDPERYDRSSQ 234  
 Db 165 VHEAPYPLFWQVLLGVAFLEGAILLCAVCRCMPCRAVADYAGTETLASPTAHLSAS 224  
 OY 235 -----RGAEDNVINEIYSILOPTQVP--EQEMEY-----QEPAPPTGVNLS 275  
 Db 225 DSAHTLLAPSSGKICTYQVGVNMTPTLSGTQEVYCGAQQPMQDLNRLGTGLAS 284  
 OY 276 PGSEHLLPEAERSQRRLVPAVEGDTETLR---QCFDDPADLVPPDSWPLMKRL 332  
 Db 285 P-----LSAP-----PA--GSPAVALQPGPOLY-DVMDAVPARMKFEVRTL 324  
 OY 333 GLMDNEIKVAKAAGHDTLYMLIKVNTGGRN 381  
 Db 325 GLREAEIEAVEICRFDDQYEMLRK--RQOQPAIGALVIAALERMG 371

## RESULT 8

O9BDP2 PRELIMINARY: PRT: 333 AA.  
 AC O9BDP2:  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE FAS antigen CD95.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-21383618; Pubmed-11491535;  
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
 RA Weiss W.R., Ansari A.A.;  
 RT "Cloning, sequencing, and homology analysis of nonhuman primate  
 Fas/Fas-ligand and co-stimulatory molecules."  
 RL Immunogenetics 53:315-328(2001).  
 DR EMBL; AF344833; AAK37529.1;  
 DR HSSP; P25445; 1DDF.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 2.







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:14:35 ; Search time 98 Seconds

(without alignments)  
102,241 Million cell updates/sec

Perfect score: 2169

Sequence: 1 MEORGNAPASGARRKRP.....HLSSGKFMYLEGNADSAXS 411

Scoring table: BLOSUM62

Gapop 10.0, -pext 0.5

Searched: 830525 segs 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq len ch: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 98

Maximum Match 100% files

Listing first 45 summs

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted of the result being printed,  
score greater than or equal to the score core distribution.  
and is derived by analysis of the total s

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	489	22.5	368	13	057408 meleagris g
2	473	21.8	368	13	09147 gallus gall
3	463	21.3	368	13	09147 gallus gall
4	285.5	13.2	438	13	09147 gallus gall
5	282	13.0	357	13	09147 gallus gall
6	233	10.7	48	4	09147 gallus gall
7	206	9.5	387	11	09147 gallus gall
8	202	9.3	333	6	09147 gallus gall
9	197	9.1	331	6	09147 gallus gall
10	196	9.0	331	6	09147 gallus gall
11	194.5	9.0	331	6	09147 gallus gall
12	194.5	9.0	331	6	09147 gallus gall
13	191.5	8.8	446	6	09147 gallus gall
14	190	8.7	413	11	09147 gallus gall
15	188.5	8.4	310	6	09147 gallus gall
16	183	8.4	328	6	09147 gallus gall

17	183	8.4	331	6	09147 gallus gall
18	181.5	8.3	327	6	09147 gallus gall
19	179.5	8.2	312	13	09147 gallus gall
20	178.5	8.2	302	13	09147 gallus gall
21	176	8.1	302	13	09147 gallus gall
22	173.5	8.0	320	6	09147 gallus gall
23	171	7.9	285	13	09147 gallus gall
24	171	7.9	319	6	09147 gallus gall
25	165.5	7.6	130	6	09147 gallus gall
26	165.5	7.6	348	12	09147 gallus gall
27	163.5	7.5	348	12	09147 gallus gall
28	163.5	7.5	349	12	09147 gallus gall
29	163.5	7.5	349	12	09147 gallus gall
30	163.5	7.5	349	12	09147 gallus gall
31	163	7.5	263	6	09147 gallus gall
32	161.5	7.4	348	12	09147 gallus gall
33	161.5	7.4	351	12	09147 gallus gall
34	160.5	7.4	349	12	09147 gallus gall
35	159	7.3	457	4	09147 gallus gall
36	157.5	7.3	349	12	09147 gallus gall
37	156.5	7.2	283	6	09147 gallus gall
38	153.5	7.1	189	6	09147 gallus gall
39	152.5	7.0	347	12	09147 gallus gall
40	152.5	7.0	351	12	09147 gallus gall
41	152	7.0	360	12	09147 gallus gall
42	149.5	6.9	355	12	09147 gallus gall
43	147.5	6.8	349	12	09147 gallus gall
44	145	6.7	347	12	09147 gallus gall
45	143.5	6.6	349	12	09147 gallus gall

## ALIGNMENTS

RESULT 1	ID	057408	PRELIMINARY:	PRT:	368 AA.
DT	01-JUN-1998	(TREMBLrel. 06, Created)			
DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)			
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)			
DE	Subgroup E ALV receptor.				
OS	Meleagris gallipavo (Common turkey).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.				
OX	NCBI_Taxid=9103;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-97471016; Pubmed-9326659;				
RA	Adkins H.B., Brojatsch J., Naughton J., Rolis M.M., Pesola J.M.,				
RA	Young J.A.;				
RT	*Identification of a cellular receptor for subgroup E avian leukosis				
RT	virus.*;				
RT	Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622(1997).				
RL	EMBL, AF006002; AAB93987.1;				
DR	HSSP; O14763; IDOG.				
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.				
DR	InterPro; IPR000485; Death				
DR	InterPro; IPR001865; Ribosomal_S2.				
DR	InterPro; IPR001368; TNFR_C6.				
DR	Pfam; PF00531; death_1.				
DR	Pfam; PF00020; TNFR_C6; 2.				
DR	SMART; SM00208; TNFR; 1.				
DR	PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.				
DR	PROSITE; PS00167; DEATH_DOMAIN; 1.				
DR	PROSITE; PS00962; RIBOSOMAL_S2_1; 1.				
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.				
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.				
DR	Receptor.				
SO	SEQUENCE				
Query Match	368 AA;	41020 MW;	5701AC2A6DAF87E2 CRC64;		
	22.5%;	Score 489;	DB 13;	Length 368;	

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:08:09 ; Search time 24 Seconds

(Without alignments)  
805.332 Million cell updates/sec

Title: US-10-052-798-1

Perfect score: 2169

Sequence: 1 MEQRGNAPASGARRKHP.....HLISGKFWYLEGNDASXS 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2135.5	98.5	440	T10B_HUMAN	O14763 homo sapien
2	1067	49.2	468	T10A_HUMAN	O00220 homo sapien
3	819.5	37.8	386	T10D_HUMAN	O9ubn6 homo sapien
4	595.5	27.5	381	T10B_MOUSE	O9gznd4 mus musculu
5	379.5	17.5	259	T10C_HUMAN	O14798 h tumor nec
6	264.5	12.2	471	T10A_BOVIN	O19131 bos taurus
7	238.5	11.0	461	T10A_PIG	P05055 sus scrofa
8	210.5	9.7	455	T10A_HUMAN	P19438 homo sapien
9	209	9.6	454	T10A_MOUSE	P25148 mus musculu
10	192	8.9	327	TNR6_MOUSE	O93038 h tumor nec
11	191	8.8	417	TNR6_HUMAN	P25445 homo sapien
12	189	8.7	335	TNR6_HUMAN	P35445 homo sapien
13	186	8.6	323	TNR6_BOVIN	P18671 bos taurus
14	179	8.3	435	TNR3_HUMAN	P36941 homo sapien
15	175.5	8.1	461	T10A_RAT	P22934 rattus norv
16	171	7.9	332	TNR6_PIG	O77736 sus scrofa
17	158	7.3	324	TNR6_RAT	O63109 rattus norv
18	152	7.0	416	T10B_CHICK	P18519 gallus gall
19	151.5	7.0	461	T10B_HUMAN	P20333 homo sapien
20	151	7.0	415	TNR3_MOUSE	P02844 mus musculu
21	146.5	6.8	351	CRMB_COMPX	O73559 compox viru
22	143.5	6.6	283	T10A_HUMAN	O92956 homo sapien
23	143.5	6.6	349	CRMB_CAMPS	O8uy21 camelopx vl
24	142.5	6.6	401	T10B_HUMAN	O00300 homo sapien
25	142.5	6.6	425	T10B_RAT	P07174 rattus norv
26	142.5	6.6	427	T10B_HUMAN	P08138 homo sapien
27	141.5	6.5	417	T10B_MOUSE	O92041 mus musculu
28	138.5	6.4	349	CRMB_VARV	P34015 variola vir
29	137	6.3	401	T10B_MOUSE	O08712 mus musculu
30	135	6.2	474	T10B_MOUSE	P25119 mus musculu
31	135	6.2	616	T10B_HUMAN	O9y66g homo sapien
32	133.5	6.2	271	TNR4_RAT	P15725 rattus norv
33	133	6.1	401	T10B_RAT	O08727 rattus norv

34	132	6.1	180	1	TR22_MOUSE	O9e62 mus musculu
35	131.5	6.1	272	1	TNR4_MOUSE	P47741 mus musculu
36	130	6.0	277	1	TNR5_HUMAN	P25942 homo sapien
37	128.5	5.9	1587	1	LMG3_HUMAN	O9y666 homo sapien
38	125.5	5.8	1581	1	LMG3_MOUSE	O9y666 mus musculu
39	124	5.7	176	1	TR23_MOUSE	O9y666 mus musculu
40	124	5.7	498	1	TNR8_MOUSE	O60846 mus musculu
41	122	5.6	300	1	TR6B_HUMAN	O95407 homo sapien
42	122	5.6	326	1	VT2_MYXL	P29825 myxoma viru
43	122	5.6	595	1	TNR8_HUMAN	P28908 homo sapien
44	121.5	5.6	2813	1	VWF_CANFA	O28295 canis famill
45	117	5.4	277	1	TNR4_HUMAN	P43489 homo sapien

## ALIGNMENTS

RESULT 1  
ID T10B\_HUMAN STANDARD: PRT: 440 AA.  
AC O14763: O14720: O15508: O15517: O15531: Q9BEVD;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL receptor-2) (TRAIL-R2)  
CN TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
[1]  
RP SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF N-TERMINUS.  
RC TISSUE=Forebrain fibroblast;  
RX MEDLINE=97459925; PubMed=9311998;  
RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y., Bolani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A., Godwin R.G., Rauch C.T.,  
RT "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL."  
RL EMO J. 16:5386-5397(1997).  
[2]  
RN SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND ALTERNATIVE SPLICING.  
RP TISSUE=Liver, and Spleen;  
RX MEDLINE=97431692; PubMed=9285725;  
RA Sreethan G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E., McMichael A.J., Bell J.I.;  
RT "TRICK2, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL."  
RL Curr. Biol. 7:693-696(1997).  
[3]  
RN SEQUENCE FROM N.A. (ISOFORM LONG), AND CHARACTERIZATION.  
RP TISSUE=Liver, and Spleen;  
RX MEDLINE=98039016; PubMed=9373179;  
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N., Tschoep J.;  
RT "Characterization of two receptors for TRAIL."  
RL FEBS Lett. 416:329-334(1997).  
[4]  
RN SEQUENCE FROM N.A. (ISOFORM SHORT).  
RP TISSUE=Ovary;  
RX MEDLINE=97467719; PubMed=9326928;  
RA Wu G.S., Burns T.F., McDonald E.R., III, Jiang W., Meng R., Splinter N.B., Markowitz S., Wu G., el-Deiry W.S.;  
RT "Killer/DR5 is a DNA damage-inducible p53-regulated death receptor gene."  
RL Nat. Genet. 17:141-143(1997).  
[5]  
RN SEQUENCE FROM N.A. (ISOFORM SHORT).  
RP MEDLINE=97390508; PubMed=9242610;  
RX Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;  
RT "An antagonist decoy receptor and a death domain-containing receptor

RT for TRAIL.";  
RL Science 277:815-818(1997).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RX MEDLINE-97467316; PubMed-9325248;  
RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,  
Cohen G.M., Alnemri E.S.;  
RT "Identification and molecular cloning of two novel receptors for the  
cytotoxic ligand TRAIL.";  
RL J Biol. Chem. 272:25417-25420(1997).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RX MEDLINE-98090092; PubMed-9430227;  
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce  
FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
RL Immunity 7:821-830(1997).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RX MEDLINE-97390509; PubMed-9242611;  
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,  
Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.;  
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy  
receptors.";  
RL Science 277:818-821(1997).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM LONG).  
RA Arii T., Akiyama Y., Okabe S., Saito K., Iwai T., Yasua Y.;  
RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2  
gene in colorectal carcinoma.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RA Cao X., Zhang W., Wan T.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RA Farrah T., Yu T., Gilbert T., Gross J., O'Hara P.;  
RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP SEQUENCE FROM N.A. (ISOFORM LONG).  
RC TISSUE=Cervix;  
RX MEDLINE-22388257; PubMed-12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Umedin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
RX MEDLINE-20017054; PubMed-10549288;  
RA Hymowitz S.G., Christinger H.W., Fuh G., Ullrich M., O'Connell M.,  
Kelley R.F., Ashkenazi A., de Vos A.M.;  
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
complex with death receptor 5.";  
RL Mol. Cell 4:563-571(1999).

RN [14]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
RX PubMed-10542098;  
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
Jones E.Y., Screaton G.R.;  
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
specificity in apoptotic initiation.";  
RL Nat. Struct. Biol. 6:1048-1053(1999).  
CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The  
adaptor molecule FADD recruits caspase-8 to the activated  
receptor. The resulting death-inducing signaling complex (DISC)  
performs caspase-8 proteolytic activation which initiates the  
subsequent cascade of caspases (aspartate-specific cysteine  
proteases) mediating apoptosis. Promotes the activation of NF-  
kappaB.  
CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- ALTERNATIVE PRODUCTS:  
Event-Alternative splicing; Named Isoforms-2;  
Name-Long; Synonyms=TRICK2B;  
Name-Short; Synonyms=TRICK2A;  
Name-Short; Synonyms=TRICK2A;  
Isoid=014763-1; Sequence=VSP\_006490;  
Isoid=014763-2; Sequence=VSP\_006490;  
CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
very highly expressed in tumor cell lines such as HeLa S3, K562,  
HL-60, SW480, A549 and G361; highly expressed in heart, peripheral  
blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
ovary, uterus, placenta, testis, esophagus, stomach and throughout  
the intestinal tract; not detectable in brain.  
CC -1- INDUCTION: TNFSF10B is regulated by the tumor suppressor p53.  
CC -1- DISEASE: Defects in TNFSF10B may be a cause of squamous cell  
carcinoma of the head and neck.  
CC -1- SIMILARITY: Contains 3 TNFR-cys repeats.  
CC -1- SIMILARITY: Contains 1 death domain.  
CC -----  
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CC -----  
DR EMBL; AF016849; AAC51778.1; -  
DR EMBL; AF018657; AAB70577.1; -  
DR EMBL; AF018658; AAB70578.1; -  
DR EMBL; AF016266; AAB81160.1; -  
DR EMBL; AF022386; AAB71949.1; -  
DR EMBL; AF012628; AAB67109.1; -  
DR EMBL; AF020501; AAB71412.1; -  
DR EMBL; AF016268; AAC01565.1; -  
DR EMBL; AF012535; AAB67103.1; -  
DR EMBL; AB014718; BAA33723.1; -  
DR EMBL; AB014710; BAA33723.1; JOINED.  
DR EMBL; AB014711; BAA33723.1; JOINED.  
DR EMBL; AB014712; BAA33723.1; JOINED.  
DR EMBL; AB014713; BAA33723.1; JOINED.  
DR EMBL; AB014714; BAA33723.1; JOINED.  
DR EMBL; AB014715; BAA33723.1; JOINED.  
DR EMBL; AB014716; BAA33723.1; JOINED.  
DR EMBL; AB014717; BAA33723.1; JOINED.  
DR EMBL; AF153687; AAF75567.1; -  
DR EMBL; AF192548; AAF07175.1; -  
DR EMBL; BC001281; AAH01281.1; -  
DR PDB; 1D0G; 22-OCT-99.  
DR PDB; 1D4V; 01-NOV-99.  
DR Genew; HGNC:11905; TNFSF10B.  
DR MIM; 603612; -  
DR MIM; 601400; -  
DR GO; GO:0016021; C:Integral to membrane; IC.  
DR GO; GO:0016506; F:apoptosis activator activity; NAS.  
DR GO; GO:0008656; F:caspase activator activity; NAS.  
DR GO; GO:0004872; F:receptor activity; NAS.

Query Match 98.5%; Score 2135.5; DB 1; Length 440;  
 Best Local Similarity 93.0%; Pred. No. 3,3e-152;  
 Matches 409; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

DB 1 MEORGNAPPAASGARRRHGPGPREARGARGLRVPTLVVAVALLVSAESALITQOD 60  
 1 MEORGNAPPAASGARRRHGPGPREARGARGLRVPTLVVAVALLVSAESALITQOD 60  
 DB 61 LAPOQAAARQOKRSSSEGLCPGGHHISEDRICISCKGQDYSTMNDLLFCLRTCD 120  
 61 LAPOQAAARQOKRSSSEGLCPGGHHISEDRICISCKGQDYSTMNDLLFCLRTCD 120  
 DB 121 SGEVEISPCPTTNTNTYCCOCEEGFREDESPKCRKRTGCGPRGMVVGDCPTMSDIECHV 180  
 121 SGEVEISPCPTTNTNTYCCOCEEGFREDESPKCRKRTGCGPRGMVVGDCPTMSDIECHV 180  
 DB 181 KE-----SGIIGTVAAVAVLVAVFVCKSLMKVY 211  
 181 KE-----SGIIGTVAAVAVLVAVFVCKSLMKVY 211  
 DB 181 KEGTGHSEAPAVEETVTSPTGPASPCSLSGIIGTVAAVAVLVAVFVCKSLMKVY 240  
 181 KEGTGHSEAPAVEETVTSPTGPASPCSLSGIIGTVAAVAVLVAVFVCKSLMKVY 240  
 DB 212 LPTLKICSGGGDPRVDRSSORPGADENVLNEIYSIIQPTVPEQEMVOPAEPTGV 271  
 212 LPTLKICSGGGDPRVDRSSORPGADENVLNEIYSIIQPTVPEQEMVOPAEPTGV 271  
 DB 241 LPTLKICSGGGDPRVDRSSORPGADENVLNEIYSIIQPTVPEQEMVOPAEPTGV 300  
 241 LPTLKICSGGGDPRVDRSSORPGADENVLNEIYSIIQPTVPEQEMVOPAEPTGV 300  
 DB 272 NMLSPGSEHLLPEPAERSQRRLVPAENEGDPTLRQCFDFADLVFDSMEPLMRK 331  
 272 NMLSPGSEHLLPEPAERSQRRLVPAENEGDPTLRQCFDFADLVFDSMEPLMRK 331  
 DB 301 NMLSPGSEHLLPEPAERSQRRLVPAENEGDPTLRQCFDFADLVFDSMEPLMRK 360  
 301 NMLSPGSEHLLPEPAERSQRRLVPAENEGDPTLRQCFDFADLVFDSMEPLMRK 360  
 DB 332 LGLMDEIVKAAEAAGHDTLYMLIKVNTKGRDASVHTLLDALETIGERLAKOIED 391  
 332 LGLMDEIVKAAEAAGHDTLYMLIKVNTKGRDASVHTLLDALETIGERLAKOIED 391  
 DB 361 LGLMDEIVKAAEAAGHDTLYMLIKVNTKGRDASVHTLLDALETIGERLAKOIED 420  
 361 LGLMDEIVKAAEAAGHDTLYMLIKVNTKGRDASVHTLLDALETIGERLAKOIED 420  
 DB 392 HLSSGKFWYLGDNADSAKS 411  
 392 HLSSGKFWYLGDNADSAKS 411  
 DB 421 HLSSGKFWYLGDNADSAKS 440  
 421 HLSSGKFWYLGDNADSAKS 440

RESULT 2  
 T10A\_HUMAN STANDARD; PRT; 468 AA.  
 AC 000220; Q96662;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10A precursor (Death  
 receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL  
 receptor 1) (TRAIL-R1).  
 GN TNFRSF10A OR DR4 OR TRAILR1 OR APO2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97238921; Pubmed-9082980;  
 RA Pan G., O'Rourke K., Chinaiyan A.M., Gentz R., Ebner R., Ni J.,  
 RA Dixit V.M.;  
 RT "The receptor for the cytotoxic ligand TRAIL.";  
 RL Science 276:111-113(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-22388257; Pubmed-12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Maruska K., Farmer A.R., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein H.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smalius D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP FUNCTION.  
 RX MEDLINE-98090092; Pubmed-9430227;  
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce  
 FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 RL Immunity 7:821-830(1997).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The  
 CC adaptor molecule FADD recruits caspase-8 to the activated  
 CC receptor. The resulting death-inducing signaling complex (DISC)  
 CC performs caspase-8 proteolytic activation which initiates the  
 CC subsequent cascade of caspases (aspartate-specific cysteine  
 CC proteases) mediating apoptosis. Promotes the activation of NF-  
 CC kappaB.  
 CC -1- SUBUNIT: Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Widely expressed. High levels are found in  
 CC spleen, peripheral blood leukocytes, small intestine and thymus,  
 CC but also in K562 erythroleukemia cells, MCF7 breast carcinoma  
 CC cells and activated T-cells.  
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.

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CC -----  
 CC EMBL: U90875; AAC51226.1; -;  
 CC DR EMBL: BC012866; AAH12866.1; -;  
 CC DR HSSP: 014763; 1D0C; TNFRSF10A.  
 CC DR Genew: HENC:11904; TNFRSF10A.  
 CC DR MIM: 603611; -;  
 CC DR GO: GO:0016021; C: integral to membrane; IC.  
 CC DR GO: GO:0016506; F: apoptosis activator activity; NAS.  
 CC DR GO: GO:0008656; F: caspase activator activity; NAS.  
 CC DR GO: GO:0005035; F: death receptor activity; TAS.  
 CC DR GO: GO:0004872; F: receptor activity; NAS.  
 CC DR GO: GO:0045569; F: TRAIL binding activity; NAS.  
 CC DR GO: GO:0007250; P: activation of NF-kappaB-inducing kinase; NAS.  
 CC DR GO: GO:0006919; P: caspase activation; NAS.  
 CC DR GO: GO:0008625; P: induction of apoptosis via death domain rec. .; NAS.  
 CC DR GO: GO:0007165; P: signal transduction; TAS.  
 CC DR InterPro: IPR004488; Death.  
 CC DR InterPro: IPR001368; TNFR\_c6.  
 CC DR Pfam: PF00531; death\_1.  
 CC DR Pfam: PF00020; TNFR\_c6; 2.  
 CC DR SMART: SM00005; DEATH; 1.  
 CC DR SMART: SM00208; TNFR; 2.  
 CC DR PROSITE: PSS0017; DEATH\_DOMAIN; 1.  
 CC DR PROSITE: PSS0052; TNFR\_NGFR\_1; 2.  
 CC DR PROSITE: PSS0050; TNFR\_NGFR\_2; 2.  
 CC KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 CC FT SIGNAL 1 23 POTENTIAL.  
 CC FT CHAIN 24 468 TUMOR NECROSIS FACTOR RECEPTOR  
 CC FT DOMAIN 24 239 SUPRANUMERARY MEMBER 10A.  
 CC FT TRANSLEM 240 262 EXTRACELLULAR (POTENTIAL).  
 CC FT DOMAIN 263 468 CYTOPLASMIC (POTENTIAL).

FT REPEAT 107 145 TNFR-CYS 1.  
 FT REPEAT 147 188 TNFR-CYS 2.  
 FT REPEAT 189 229 TNFR-CYS 3.  
 FT DOMAIN 365 448 DEATH.  
 FT DOMAIN 29 332 POLY-ALA.  
 FT DISULFID 132 145 BY SIMILARITY.  
 FT DISULFID 148 164 BY SIMILARITY.  
 FT DISULFID 167 180 BY SIMILARITY.  
 FT DISULFID 170 188 BY SIMILARITY.  
 FT DISULFID 190 204 BY SIMILARITY.  
 FT DISULFID 207 221 BY SIMILARITY.  
 FT DISULFID 211 229 BY SIMILARITY.  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 141 141 H -> R (IN REF. 1).  
 FT CONFLICT 209 209 R -> T (IN REF. 1).  
 SO SEQUENCE 468 AA; 50061 MW; 7E9661859A550C4 CRC64;  
 Query Match 49.28; Score 1067; DB 1; Length 468;  
 Best Local Similarity 54.68; Pred. No. 2.2e-72;  
 Matches 233; Conservative 39; Mismatches 115; Indels 40; Gaps 8;  
 QY 5 GONAPASGARRRGPGPREARGARPLGRVPTLVVAVNLL-LVSAESALITQDLAP 63  
 DB 60 GQHEPSAR-ARAGRAPGPRRPREASPLRVHKTFRFVVGVLQVPSAATIKLHD-- 115  
 QY 64 QORAPPOQRSSPESEGLCPGHHISEGDRDCISCKYGODYSTHNDLLFCLCTRCDSGE 123  
 DB 116 -QSIGTQOWEHSPIGELCPGSHSEHRCACNCTBEVGYTNASNNLFACLPCTACKSDE 174  
 QY 124 VEISPTTTRNTVCCCEGTFREDSPEMCKCTGCPGMVKGVDCTPMSDIECVHKS 183  
 DB 175 EERSPTTTRNTACQCKPGTFRRDNSAEMCKCSRCGPMVKGVDCTPMSDIECVHKS 234  
 QY 184 G-----IIIGVVAAVLVAVVCAVCSLMMKVLPTLKGIC-----SGGGDPERVDSS 233  
 DB 235 GNGNINIVLVTLVVELLVAVLT-----VCCITSGCGGDPKCMQVVC 279  
 QY 234 -----QRRGAEDNVLNEIVSILQ--PTQVPEQEMVEQPEPTGVNMLSGESEHLE 284  
 DB 280 FWRLLGRGGAEDNANHEILSNADSLSTFVSEQMSQSEPADLGTVYSPGACQLTG 339  
 QY 285 PAERASORRRLLVPAHEGPTETLRQCFDFADLVFPDSPEPLMKLMDNEIKYAKA 344  
 DB 340 PAEEGSSORRRLLVPAAGADPTETLMLEPFKFNIVPFDSDQKRLDLTKNEIDVRA 399  
 QY 345 EAAGHRDTLYTMLIKVNTKGRDASVHTLDALETLEERLAKOKIEHLLSSGFYLEG 404  
 DB 400 GTAGPGALYAMLKWKNTGRNASHTLLDALERMERAKKXIQDLVDGKFTLED 459  
 QY 405 NADSAS 411  
 DB 460 GTGSASV 466  
 RESULT 3  
 T10D\_HUMAN  
 ID T10D\_HUMAN STANDARD; PRT; 386 AA.  
 AC OSUBN6; O9Y6G4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10D precursor (Decoy receptor 2) (DcR2) (TNF-related apoptosis-inducing ligand receptor 4) (TRAIL receptor-4) (TRAIL-R4) (TRAIL receptor with a truncated death domain)  
 GN TNFRSF10D OR DCR2 OR TRAILR4 OR TRUND.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND VARIANT.  
 RC TISSUE=fetal lung;

RX MEDLINE=98044290; PubMed=9382840;  
 RA Marsters S.A., Sheridan J.P., Pitti R.M., Huang A., Skubatch M.,  
 RA Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P.,  
 RA Ashkenazi A.,  
 RT "A novel receptor for Apo2L/TRAIL contains a truncated death domain."  
 RL Curr. Biol. 7:1003-1006(1997).  
 RP [2]  
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND VARIANTS SER-35 AND LEU-310.  
 RC TISSUE=Forebrain fibroblast, and peripheral blood lymphocytes;  
 RX MEDLINE=98090091; PubMed=9430226;  
 RA Degli-Esposti M.A., Dougall W.C., Smolak P.J., Waugh J.Y., Smith C.A.,  
 RA Goodwin R.G.,  
 RT "The novel receptor TRAIL-R4 induces NF-kappaB and protects against TRAIL-mediated apoptosis, yet retains an incomplete death domain."  
 RL Immunity 7:813-820(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RX MEDLINE=98196860; PubMed=9537512;  
 RA Pan G., Ni J., Yu G.-L., Wei Y.-F., Dixit V.M.,  
 RT "TRUND, a new member of the TRAIL receptor family that antagonizes TRAIL signalling."  
 RL FEBS Lett. 424:41-45(1998).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Contains a truncated death domain and hence is not capable of inducing apoptosis but protects against TRAIL-mediated apoptosis. Reports are contradictory with regards to its ability to induce the NF-kappaB pathway (According to Ref.1 it cannot but according to Ref.2 it can induce the NF-kappaB pathway).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Widely expressed, in particular in fetal kidney, lung and liver, and in adult testis and liver. Also expressed in peripheral blood leukocytes, colon and small intestine, ovary, prostate, thymus, spleen, pancreas, kidney, lung, placenta and heart.  
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
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 CC EMBL: AF029761; AAD03477.1; -  
 CC EMBL: AF021232; AAC32765.1; -  
 CC EMBL: AF021233; AAC32766.1; -  
 CC EMBL: AF023849; AAC52053.1; -  
 CC HSSP: O14763; 1D4V.  
 CC DR GeneW; HGNC:11907; TNFRSF10D.  
 CC DR MIM: 603614; -  
 CC DR InterPro: IPR001368; TNFR-C6.  
 CC DR Pfam: PF00020; TNFR\_C6; 2.  
 CC DR SMART: SM00208; TNFR; 2.  
 CC DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 CC DR PROSITE: PS0050; TNFR\_NGFR\_2; 2.  
 CC DR Receptor: Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;  
 CC KW Polymorphism.  
 CC FT SIGNAL 1 55  
 CC FT CHAIN 56 386  
 CC FT DOMAIN 56 211 TUMOR NECROSIS FACTOR RECEPTOR  
 CC FT TRANSMEM 212 232 SUPERFAMILY MEMBER 10D.  
 CC FT DOMAIN 233 386 EXTRACELLULAR (POTENTIAL).  
 CC FT REPEAT 38 97 CYTOPLASMIC (POTENTIAL).  
 CC FT REPEAT 98 139 TNFR-CYS 1.  
 CC FT REPEAT 140 180 TNFR-CYS 2.  
 CC FT DOMAIN 340 366 TNFR-CYS 3.  
 CC FT DOMAIN 225 228 DEATH (TRUNCATED).  
 CC FT DOMAIN 246 250 POLY-VAL.  
 CC FT DISULFID 83 96 POLY-CYS.  
 CC FT DISULFID 99 115 BY SIMILARITY.

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FT DISULFID 118 131 BY SIMILARITY.
FT DISULFID 121 139 BY SIMILARITY.
FT DISULFID 141 155 BY SIMILARITY.
FT DISULFID 158 172 BY SIMILARITY.
FT DISULFID 162 180 BY SIMILARITY.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 35 35 P -> S (IN TRAIL-R4-B).
FT VARIANT 310 310 /FTID=VAR.011417.
FT VARIANT 310 310 S -> L (IN TRAIL-R4-B).
FT FT /FTID=VAR.011418.
SQ SEQUENCE 386 AA; 41823 MW; 77A93577CAAF2632 CRC64;

Query Match 37.8%; Score 819.5; DB 1; Length 386;
Best Local Similarity 43.7%; Pred. No. 5.4e-54;
Matches 193; Conservative 36; Mismatches 116; Indels 97; Gaps 5;

OY 5 GONAPASGARKRHGPGPREARGAPGLRVPKTL-VLVVAVALLLVASASALITQODLA 62
5 GGSVTPASSARAGRYPCARTASGRPWLDPKILKEVVFIVAVLLPVVDASATIPRODEV 64
DB 63 PQRAPRQQRSPSEGLCPRGHHSIDGDCISCKGODYSTHMDLFLCLCTRCDSG 122
65 PQQVAPRQQRSLKEECPAGSHREYTGACNPCTEGVDYTIASNNLPSCLLCTYCKSG 124
OY 123 EVELSPCTTRNTVCOCEEGTFREDESPCMCRKCRPGMWKVGDCPTMWDIECVHKE 182
125 QTKKSSCTTRTDVCOCEKSGFQDKNSPEKCRICRGCPGMKVNKCTPRSDICKNES 184
OY 183 SGIIIGTVAA-----VVLIVAFYCKSLMKKVLPLYKGC 219
185 AASSTGTPAAEEVTTILGLMASPHYLIITIVLITLAVVVGFSCRKFTSYLKGIC 244
OY 220 SGGGSGDEPERDR-----SSORPCAEADVNLAEIYS--ILQTPVPEQMEVQEPAPPT 269
245 SGGGSGGGERVHRYLFRRRSCPSRVPAGADNARNETISNRYLOPTQVSEQICQCELAELT 304
OY 270 GYVNLSPGSEHLEPAEAERSORRLVLPANEGDPETLRQCFEDPADLVPPDSWPELM 329
305 GYVNPSPPEPRLLEQAEAGCCORRLVLYVND----- 339
DB 330 RKLGLMDNEIKVAKAEAGHRTLYTMLIKVKNKGRDASVHLLDALETLGERLAKOKI 389
340 -----SADISTLLDASATLSEGHAKETI 362
OY 390 EDHLLSGKFMYLEGNADSAXS 411
363 QDOLVGSEKLFYEDEGSAFS 384

RESULT 4
ID T10B_MOUSE STANDARD; PRT; 381 AA.
AC Q9QZM4; Q9JUL5; Q9JUL6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (MK).
GN TNFRSF10B OR DR3 OR KILLER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99310501; Pubmed=10383128;
RA Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;
RT "Molecular cloning and functional analysis of the mouse homologue of the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand (TRAIL) death receptor.";
RL Cancer Res. 59:2770-2775(1999).

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Nakamura Y., Tamari M., Watanabe O.;
RT "Mouse TRAIL receptor.";
RX Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFRSF10/TRAIL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-kappaB.
CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.
CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -1- SIMILARITY: Contains 1 death domain.
CC -----
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CC -----
DR EMBL: AF176833; AAD52656.1;
DR EMBL: AB031081; BAA96462.1;
DR EMBL: AB031082; BAA96463.1;
DR HSP: O14763; IDOG.
DR MGD: MGI:1341090; Tnfrsf10b.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR SMART: PR00020; TNFR_c6; 2.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PSS0017; DEATH_DOMAIN; 1.
DR PROSITE: PSS00652; TNFR_NGFR_1; 2.
DR PROSITE: PSS0050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Transmembrane; Repeat; Signal.
FT SIGNAL 1 52
FT CHAIN 53 381
FT DOMAIN 53 160
FT TRANSMEM 161 181
FT DOMAIN 182 381
FT REPEAT 26 86
FT REPEAT 87 129
FT REPEAT 130 169
FT DOMAIN 273 356
FT DISULFID 74 85
FT DISULFID 88 105
FT DISULFID 108 121
FT DISULFID 111 129
FT DISULFID 131 145
FT DISULFID 148 161
FT DISULFID 151 169
FT CONFLICT 42 42
FT CONFLICT 97 97
FT CONFLICT 128 128
FT CONFLICT 180 180
FT CONFLICT 187 187
FT CONFLICT 215 215
FT CONFLICT 229 229
FT CONFLICT 306 306
SQ SEQUENCE 381 AA; 42223 MW; 2F7999EA2EB485B1 CRC64;

Query Match 27.5%; Score 595.5; DB 1; Length 381;
Best Local Similarity 35.6%; Pred. No. 2.8e-37;

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QY 212 LPYLKICSGGG-----GDEPRVDRS-----SORPGADNVLNEIVS----- 248  
 Db 240 -PKYSLICGOSTLVKGEPELVLPARGFNPTTICSSSPSSPSVPIPIISCDRBNFG 298  
 QY 249 -IIQPIOV-----PEQEMEVOEPAEPTGVNMLSPG--ESEHLLPEAEERS 291  
 Db 299 AVASPSSEETAPRLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEA 358  
 QY 292 QRRRLVLPANEGDPTETLRQCFDPAFLVPDSEPELRKLGMDNITKAAKAAAGH-R 350  
 Db 359 SAPSAPQDLADADA-FLYAVVDG-----VPPSRKKELVRRGLGSEHIELEENGSHLR 413  
 QY 351 DTLVTMLIKWVNT-----GRDASYHTLLDALETIGERL---AKOKIEDHL 394  
 Db 414 EAQYSMLAAMRRRRRREARETLELLGRVLRMDLLGCLLENIEALGAARLASERLL 470

RESULT 7  
 ID TRIA\_PIG STANDARD; PRT; 461 AA.  
 AC P50555;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 13-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 GN TNFRSF1A OR TNFR1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_Taxid:9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=96011645; PubMed=7590278;  
 RA Suter B., Pauli U.H.;  
 RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor  
 receptor.";  
 RL Gene 163:263-266(1995).  
 CC -1- FUNCTION: Receptor for TNFRSF2/TNF-alpha and homotrimeric  
 CC TNFRSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (By similarity).  
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to  
 CC homotrimerization. The aggregated death domains provide a novel  
 CC molecular interface that interacts specifically with the death  
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
 CC RIP and possibly FADD, are recruited to the complex by their  
 CC association with TRADD. This complex activates at least two  
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
 CC Binds BAG4 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL, U19994; AAC48499.1; -;  
 DR PIR, JC4302; JC4302.  
 DR HSSP, P19438; 1TNR.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam, PF00531; death; 1.  
 DR Pfam, PF00020; TNFR\_c6; 3.

DR SMART, SM00005; DEATH; 1.  
 DR SMART, SM00208; TNFR; 4.  
 DR PROSITE, PS00652; TNFR\_NGFR.1; 3.  
 DR PROSITE, PS00650; TNFR\_NGFR.2; 2.  
 DR PROSITE, PS50017; DEATH\_DOMAIN; 1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 461  
 FT TRANS 22 210  
 FT DOMAIN 211 233  
 FT TRANS 234 461  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 195  
 FT DOMAIN 340 350  
 FT DOMAIN 362 447  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 123  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 194  
 FT DISULFID 185 190  
 FT CARBOHYD 54 54  
 FT CARBOHYD 86 86  
 FT CARBOHYD 145 145  
 FT CARBOHYD 151 151  
 SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

Query Match 11.08; Score 238.5; DB 1; Length 461;  
 Best Local Similarity 24.48; Pred. No. 1.6e-10;  
 Matches 117; Conservative 58; Mismatches 164; Indels 141; Gaps 26;

QY 30 PGLRVPPTLVVVAALVLLV---SASEALLTQDLAQQAQAQKSSSE-----GLC 81  
 Db 7 PGLLP---LVLRALLVDVYPAGVHGLVHPGREGRESLCPQKYSHPQNSICCTKC 62  
 QY 82 PPGHISED-----GRDCISCKYGODYSHWMDLFLCETRODS--GEVELSPCTTR 133  
 Db 63 HKGTYLINDGLGRLDPCRECDNG-FTYASENHLTQCLSCSKRSMGSEVLSPECTVOR 121  
 QY 134 NTVCQCEGTFFREDSPEM--CRKCRTPGCPRGVNVKGDCTPWSIDECVHRESGIIIT-- 187  
 Db 122 DTVOGCRKNQYRKWSETELPQCLNCSL-CBNGTYQL-PCLEKODTIC-NCHSGFLADKE 178  
 QY 188 -----GVTYAAVLLI-----VAVFV-----CSSLW 208  
 Db 179 CVSCVNCNKNCKNLCPATSETRNDPQDTGTVLLPLVIEFGCLAFELVGLACRYQRW 238  
 QY 209 KKVLPYLKICSGGG-----GDEPRVDRS-----SORPGADNVLNEIVSIL 250  
 Db 239 K---PKYSLICGOSTLVKGEPELVLPARGFNPTTICSSSPSSPSVPIPIISCDRBNFG 298  
 QY 251 QPIQVP--EQEMEVOEPAE-----PTGVNMLSP-----GESEHLLPEAE 288  
 Db 296 SPFTTFCDDMSNINIKYTSPPKEIAPPQAGPILPMPASTVPVPLPKMGSAHSAHSA 355  
 QY 289 ERSQRRLLVLPANEGDPTETLRQCFDPAFLVPDSEPELRKLGMDNIT-KVAAKAA 347  
 Db 356 QLA-----DADA-FLYAVVDG-----VPPSRKKEVRLGLGSEHIELEENG 400  
 QY 348 GHRDTLYTMLIKWVNT-----GRDASYHTLLDALETIGERL---AKOKIEDHL 394  
 Db 401 CLREAOYSMLAAMRRRRRREARETLELLGRVLRMDLLGCLLENIEALRGARLAPAPHL 460

RESULT 8  
ID TRIA\_HUMAN STANDARD: PRT: 455 AA.  
AC P19438;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
DE (TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor  
binding protein 1 (TRAF1)].  
GN TNFRSF1A OR TNFR1 OR TNFRAR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=90235285; PubMed=2158863;  
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Mong G.H.W.,  
RA Geranaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;  
RT "Molecular cloning and expression of a receptor for human tumor  
necrosis factor.";  
RL Cell 61:361-370(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90235284; PubMed=2158862;  
RA Loetscher H., Pan Y.-C.E., Lamm H.-W., Gentz R., Brockhaus M.,  
RA Tabuchi H., Lesslauer W.;  
RT "Molecular cloning and expression of the human 55 kd tumor necrosis  
factor receptor.";  
RL Cell 61:351-359(1990).  
RN [3]  
RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.  
RX MEDLINE=91006021; PubMed=1698610;  
RA Nopfer Y., Kemper O., Brakebusch C., Engelmann H., Zwarg R.,  
RA Aderka D., Holtmann H., Wallach D.;  
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA  
for the type I TNF-R, cloned using amino acid sequence data of its  
soluble form, encodes both the cell surface and a soluble form of the  
receptor.";  
RL EMBO J. 9:3269-3278(1990).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91090841; PubMed=1702293;  
RA Himmeler A., Nauber-Fogy I., Kroenke M., Scheurich P., Pfitzenmaier K.,  
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
RT "Molecular cloning and expression of human and rat tumor necrosis  
factor receptor chain (p60) and its soluble derivative, tumor  
necrosis factor-binding protein.";  
RL DNA Cell Biol. 9:705-715(1990).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=91017509; PubMed=2170974;  
RA Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;  
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
expression of recombinant soluble TNF-binding protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92250049; PubMed=1315717;  
RA Fuchs P., Stehl S., Dworzak M., Himmeler A., Ambros P.F.;  
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
localization to chromosome 12p13.";  
RL Genomics 13:219-224(1992).  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
RA Rajkumar N.R., Toch E.J., Yi Q., Nickerson D.A.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buelow R.H., Schaefer C.F., Bat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Dichtenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [9]  
RP SEQUENCE OF 41-45.  
RX MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
urine. Evidence for immunological cross-reactivity with cell surface  
tumor necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536(1990).  
RN [10]  
RP INTERACTION WITH BAG4.  
RX MEDLINE=99115917; PubMed=9915703;  
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;  
RT "Prevention of constitutive TNF receptor 1 signaling by silencer of  
death domains.";  
RL Science 283:543-546(1999).  
RN [11]  
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
RX MEDLINE=93258809; PubMed=8387891;  
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,  
RA Broger C., Loetscher H., Lesslauer W.;  
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
beta complex: implications for TNF receptor activation.";  
RL Cell 73:431-445(1993).  
RN [12]  
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
RX MEDLINE=97094982; PubMed=8939750;  
RA Naismith J.H., Devine T.O., Khono H., Sprang S.R.;  
RT "Structures of the extracellular domain of the type I tumor necrosis  
factor receptor.";  
RL Structure 4:1251-1262(1996).  
RN [13]  
RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
RX MEDLINE=99213501; PubMed=10199409;  
RA McDermott M.F., Aksentjevich I., Galon J., McDermott E.M.,  
RA Ogunkolade B.W., Centola M., Mansfield E., Giedda M., Karenko L.,  
RA Petersson T., McCarthy J., Frucht D.M., Ainger M., Torosyan Y.,  
RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,  
RA Schliengen R., Kumarejewa T.R., Cooper S.M., Vella J.P., Amos C.I.,  
RA Mulvey J., Quane K.A., Molloy M.G., Rinaldi A., Powell R.J.,  
RA Hitman G.A., O'Shea J., Kastner D.L.;  
RT "Germline mutations in the extracellular domains of the 55 kDa TNF  
receptor, TNFR1, define a family of dominantly inherited  
autoinflammatory syndromes.";  
RL Cell 97:133-144(1999).  
RN [14]  
RP FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
TNFSF1/Lymphotoxin-alpha. The adaptor molecule FADD recruits  
caspase-8 to the activated receptor. The resulting death-inducing  
signaling complex (DISC) performs caspase-8 proteolytic activation  
which initiates the subsequent cascade of caspases (aspartate-  
specific cysteine proteases) mediating apoptosis. Contributes to  
the induction of noncytotoxic TNF effects including anti-viral

CC state and activation of the acid sphingomyelinase.  
 CC - SUBUNIT: Binding of TNF to the extracellular domain leads to  
 CC homotrimerization. The aggregated death domains provide a novel  
 CC molecular interface that interacts specifically with the death  
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
 CC RIP and possibly FADD, are recruited to the complex by their  
 CC association with TRADD. This complex activates at least two  
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
 CC Binds BAG4.  
 CC SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
 CC - DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO  
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH  
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
 CC - PUT: The soluble form is produced from the membrane form by  
 CC proteolytic processing.  
 CC - DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
 CC familial hibernian fever (FHF), a disease characterized by  
 CC recurrent fever, abdominal pain, localized tender skin lesions and  
 CC myalgia.  
 CC - SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC - SIMILARITY: Contains 1 death domain.  
 CC - DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".  
 CC -----  
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 CC -----  
 DR EMBL: X55313; CAA39021.1; -  
 DR EMBL: M33294; AAA03210.1; -  
 DR EMBL: M58286; AAA36753.1; -  
 DR EMBL: M63121; AAA36754.1; -  
 DR EMBL: M73866; AAA61201.1; -  
 DR EMBL: M75865; AAA61201.1; JOINED.  
 DR EMBL: M60275; AAA36756.1; -  
 DR EMBL: A21522; CAA01558.1; -  
 DR EMBL: A131997; AAM77802.1; -  
 DR EMBL: BC010140; AAH10140.1; -  
 DR PIR: A38208; GQH0T1.  
 DR PDB: 1TNR; 31-JUL-94.  
 DR PDB: 1NCF; 07-DEC-95.  
 DR PDB: 1EXT; 11-JAN-97.  
 DR PDB: 1FT4; 12-OCT-01.  
 DR PDB: 1TCH; 01-APR-02.  
 DR GeneW: HGNC:11916; TNFRSF1A.  
 DR MIM: 191190; -  
 DR MIM: 142680; -  
 DR GO: GO:0005576; C:extracellular; TAS.  
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO: GO:0005033; F:tumor necrosis factor receptor, type I actl. . .; TAS.  
 DR GO: GO:0007165; P:signal transduction; TAS.  
 Query Match 9.7%; Score 210.5; DB 1; Length 455;  
 Best Local Similarity 22.5%; Pred. No. 2e-08;  
 Matches 104; Conservative 60; Mismatches 160; Indels 139; Gaps 22;

QY 167 VGDCTPMSD-----IEC-----VHKESGIIIGVTAAVVLIIVAVFC-KSL----- 207  
 DB 176 ENECSCNCKKSLECTCLCPQIENVKGTEDSGTIVLPIVIFGCLLSLITGLMYR 235  
 QY 208 ---WKVLPYIKGICSGGGGDPER---VDRSSQPGADNVLNETIVSLQPTQPEQME 261  
 DB 236 YQWMSKSLYST--VC--GKSTPEKEGEGTTRPLAPNPFSP-----TPGFTPLGFS 286  
 QY 262 VOEPAEPGVNMLSPGSEHILLEPAEARSQRRLLVPANG-----DPTETLR 310  
 DB 287 PVPSTFTYSSSTYPGDCPNRAP-----REVAPYGGADPILATALASDTPNPL 338  
 QY 311 QCFDFA-----DLYPFDSPWEIMKRLGMDNEI-KVAKAAAGHRD 351  
 DB 339 QKMEISAHKPSLDTPDPAITLYAVENPPLRWKEFVARLDSDEIDRLQNGRCIRE 398  
 QY 352 TLYTMLIKVVKNT-----GRDASVHPLDALFTLGERL 384  
 DB 399 AQYSMLATWRRTTREPREATLEILGRVLRMDLGLCTEDIEBAL 441  
 RESULT 9  
 TR1A\_MOUSE STANDARD: PRT; 454 AA.  
 AC P25118;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R1) (p55).  
 GN TNFRSF1A OR TNFR1 OR TNFR-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=91187885; PubMed=1849278;  
 RX Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wong G.H., Chen E.Y., Goeddel D.V.,  
 RT "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=91246168; PubMed=1645445;  
 RX Goodwin R.G., Anderson D., Jerzy R., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.";  
 RL Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=91285014; PubMed=1647956;  
 RX Barrett K., Taylor-Fiswick D.A., Cope A.P., Kisonergis A.M.,  
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;  
 RT "Cloning, expression and cross-linking analysis of the murine p55  
 RT tumor necrosis factor receptor.";  
 RL Eur. J. Immunol. 21:1649-1656(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Tissue=Spleen;  
 RX MEDLINE=92039815; PubMed=1657766;  
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;  
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";  
 RN Immunogenetics 34:338-340(1991).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94245292; PubMed=8188324;  
 RA Bebo B.F., Linthicum D.S.;  
 RT "Nucleotide sequence of the TNF type I receptor from a mouse  
 RT endothelioma cell line.";

RL Immunogenetics 39:450-451(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93156721; PubMed-8381516;  
 RA Rothe J., Bluetmann H., Gentz R., Lesslauer W., Steinmetz M.:  
 RT "Genomic organization and promoter function of the murine tumor  
 RL necrosis factor receptor beta gene.";  
 RN Mol. Immunol. 30:165-175(1993).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-22368257; PubMed-12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Stajich M.J., Utsid T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Rahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.:  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [1]  
 CC -1- FUNCTION: Receptor for TNFR2/TNF-alpha and homotrimeric  
 CC TNFR1/Lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-activation  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (By similarity).  
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to  
 CC homotrimerization. The aggregated death domains provide a novel  
 CC molecular interface that interacts specifically with the death  
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,  
 CC RIP and possibly FADD, are recruited to the complex by their  
 CC association with TRADD. This complex activates at least two  
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.  
 CC -1- BINDS BAG4 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
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 CC EMBL: M60468; AAA39751.1; -  
 CC EMBL: M59377; AAA40464.1; -  
 CC EMBL: X59238; CAA41922.1; -  
 CC EMBL: X57796; CAA40936.1; -  
 CC EMBL: L26349; AAA59361.1; -  
 CC EMBL: M76656; AAA40465.1; -  
 CC EMBL: M88067; AAA40465.1; JOINED.  
 CC EMBL: M76655; AAA40465.1; JOINED.  
 CC EMBL: BC004599; AAH04599.1; -  
 CC EMBL: BC004599; AAH04599.1; -  
 CC EMBL: A38634; GQMS1.1.  
 CC HSP: P19438; 1EXT.  
 CC MGD: MGI:1314884; Tnf:tnfr1.  
 CC GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.  
 CC GO: GO:0006952; P:defense response; IMP.  
 CC GO: GO:0006954; P:inflammatory response; IMP.  
 CC GO: GO:0007515; P:lymph gland development; IMP.

DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS00650; TNFR\_NGFR\_2; 3.  
 DR PROSITE: PS0017; DEATH\_DOMAIN; 1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 454  
 FT DOMAIN 22 212  
 FT TRAMEM 213 235  
 FT DOMAIN 236 454  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 339 349  
 FT DOMAIN 356 441  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 195  
 FT CARBOHYD 185 191  
 FT CARBOHYD 191 191  
 FT CARBOHYD 151 151  
 FT CARBOHYD 202 202  
 FT CONFLICT 394 394  
 SO SEQUENCE 454 AA; 50129 MW; 0710C2BEC3C2BBD9 CRC64;  
 Query Match 9.6%; Score 209; DB 1; Length 454;  
 Best Local Similarity 21.5%; Pred. No. 2,6e-08;  
 Matches 105; Conservative 58; Mismatches 137; Indels 188; Gaps 24;  
 31 GLRVPRTIVYVNAVLIVSASALITQODLAQQAQAQKSSPSBGLCPGCHIT--- 87  
 2 GLRTPGLLSTLVLLALMLGTHPSGVY--GLVPS--LGDEKRDS---LCPGKRYVHSH 53  
 88 -----SEDGRD--CISCKRGDYSTHMDLFLCLRCTRC--DSGEV 124  
 54 NNSICCTKCHKGYLVSDCPSPGRDVCRCENG--FTASQNLRLROCLSKCTKREMSQV 112  
 125 ELSPCTTNTNTVQCCEBGTFRBEDSPM-----CRKCRFG-----CPRG- 163  
 113 EISPCADKDTVCCKENOFORYLSETHFOCVDCSCFNGTWTIPCKETONTVCNCHAGP 172  
 164 MVKVGCTPMS-----DIECHN-----KESG-----IIGVYAAAVLV 198  
 173 FLRESFVPCSHCKKNECKKLCPLPPLNVTNPQDSGAVALLPLVILGLCLLSFTI- 231  
 199 AVFVCKSLMLKKVLPYLKIGSGGGGDPDERVDRSSORPGAEDVNLVEISIILOTPVPPQ 258  
 232 -SLMCHYPRV-----TGTV-----MSPGSE-----HLEPAEAE 289  
 259 EMEVQEPAP-----TGTV-----MSPGSE-----HLEPAEAE 289  
 257 EERAGKPLPAPSPAPSP 315  
 290 RSORRLILVANGCD-----PTETLRQCFDFEA-----LLVPE 322  
 316 -----VPTGADPLLESLSVAPAPTSVQWESAIHPQRPNADLAIVAVVGVP 368  
 323 DSWEPLMRKLGIMDNEI-KVAKAEAGHRDTLTMLIKWNKGRDASVHTLLDAETLG 381

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DB      369  ARWKEFRMFGLSEHIERLEEMONGRCIJEAOYSMLLEAWRRRTPRHE-----DTLEVVG 422
OY      382  ERLAKOKI 389
DB      423  LVLSKMANL 430

RESULT 10
TNRF6_MOUSE STANDARD: PRT: 327 AA.
ID      TNRF6_MOUSE
AC      P25446; O8DCQ1;
DT      01-MAY-1992 (Rel. 22, Created)
DT      01-MAY-1992 (Rel. 22, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE      receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE      (CD95).
CN      TNFRSF6 OR APT1 OR FAS.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92148151; PubMed=1371136;
RA      Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Yonehara S.,
RA      Copeland N.G., Jenkins N.A., Nagata S.;
RT      "The CDNA structure, expression, and chromosomal assignment of the
RT      mouse Fas antigen.";
RL      J. Immunol. 148:1274-1279(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      STRAIN=129/SV;
RA      Koczan D., Ibrahim S.M., Thiesen H.J.;
RT      "Role of a mutant fas receptor in a transgenic mouse.";
RL      Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RX      STRAIN=C57BL/6J; TISSUE=Kidney;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nakado T., Pesole G., Quackenbush J.,
RA      Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereis P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Winking L.,
RA      Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
RN      [4]
RP      SEQUENCE OF 1-96 FROM N.A.
RX      MEDLINE=93189576; PubMed=7680478;
RA      Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT      "Aberrant transcription caused by the insertion of an early
RT      transposable element in an intron of the Fas antigen gene of lpr
RT      mice.";
RL      Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN      [5]
RP      INTERACTION WITH DAXX.
RX      MEDLINE=97358533; PubMed=9215629;
RA      Yang X., Khosravi-Far R., Chang H.Y., Baltimore D.;

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RT      "Daxx, a novel Fas-binding protein that activates JNK and apoptosis.";
RL      Cell 89:1067-1076(1997).
RN      [6]
RP      VARIANT LPR.
RX      MEDLINE=92195401; PubMed=1372394;
RA      Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA      Nagata S.;
RT      "Lymphoproliferation disorder in mice explained by defects in Fas
RT      antigen that mediates apoptosis.";
RL      Nature 356:314-317(1992).
CC      -I- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC      recruits caspase-8 to the activated receptor. The resulting death-
CC      inducing signaling complex (DISC) performs caspase-8 proteolytic
CC      activation which initiates the subsequent cascade of caspases
CC      (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC      mediated apoptosis may have a role in the induction of peripheral
CC      tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC      both (By similarity).
CC      -I- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC      -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -I- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC      LIVER, LUNG, HEART, AND ADULT OVARY.
CC      -I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC      AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC      -I- DISEASE: DEFECTS IN TNFRSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC      DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC      PRODUCTION.
CC      -I- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC      -I- SIMILARITY: Contains 1 death domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: M83649; AAA37593.1; -
DR      EMBL: AK002590; BAB22211.1; -
DR      EMBL: AJ295702; CAC00638.1; -
DR      EMBL: AJ295703; CAC00638.1; JOINED.
DR      EMBL: AJ295704; CAC00638.1; JOINED.
DR      EMBL: S56490; AAB25700.1; -
DR      EMBL: S56485; AAB25700.1; JOINED.
DR      EMBL: S56486; AAB25700.1; JOINED.
DR      PIR: A46484; A46484.
DR      HSSP: P25445; IDDF.
DR      MGD: MGI:95484; Tnfrsf6.
DR      InterPro: IPR000488; Death.
DR      InterPro: IPR001368; TNFR_c6.
DR      Pfam: PF00531; death.1.
DR      Pfam: PF00020; TNFR_c6; 3.
DR      SMART: SM00005; DEATH; 1.
DR      SMART: SM00208; TNFR; 3.
DR      PROSITE: PS00652; TNFR_NGFR.1; 2.
DR      PROSITE: PS50050; TNFR_NGFR.2; 2.
DR      PROSITE: PS50017; DEATH_DOMAIN; 1.
KW      Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW      Disease mutation.
FT      SIGNAL 1 21
FT      CHAIN 22 327
FT      DOMAIN 22 169
FT      TRANSMEM 170 186
FT      DOMAIN 187 327
FT      REPEAT 43 79
FT      REPEAT 80 123
FT      REPEAT 124 162
FT      DOMAIN 222 306
FT      DISULFID 44 55
FT      DISULFID 56 69
FT      FT 78

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CC Isoid=093038-1; Sequence=Displayed;  
 CC Name=2; Synonyms=LARD-1B;  
 CC Isoid=093038-2; Sequence=VSP\_006504;  
 CC Name=3; Synonyms=WSL-S1, LARD-3;  
 CC Isoid=093038-3; Sequence=VSP\_006497, VSP\_006499;  
 CC Name=4; Synonyms=WSL-S2, LARD-2;  
 CC Isoid=093038-4; Sequence=VSP\_006501, VSP\_006502;  
 CC Name=5; Synonyms=LARD-4, LARD-11;  
 CC Isoid=093038-5; Sequence=VSP\_006495;  
 CC Name=6; Synonyms=LARD-5;  
 CC Isoid=093038-6; Sequence=VSP\_006491, VSP\_006495;  
 CC Name=7; Synonyms=LARD-6;  
 CC Isoid=093038-7; Sequence=VSP\_006491, VSP\_006494;  
 CC Name=8; Synonyms=LARD-7;  
 CC Isoid=093038-8; Sequence=VSP\_006492;  
 CC Name=9; Synonyms=LARD-8;  
 CC Isoid=093038-9; Sequence=VSP\_006491;  
 CC Name=10; Synonyms=LARD-9;  
 CC Isoid=093038-10; Sequence=VSP\_006503;  
 CC Name=11; Synonyms=Beta;  
 CC Isoid=093038-11; Sequence=VSP\_006496;  
 CC Name=12; Synonyms=Beta soluble;  
 CC Isoid=093038-12; Sequence=VSP\_006499, VSP\_006500;  
 CC TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS, COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.  
 CC -1- PPM: GLYCOSYLATED (PROBABLE).  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
 CC -1- CAUTION: Ref:5 reports for isoform 4 at position 208 a serine residue instead of arginine.  
 CC -----  
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 CC -----  
 DR EMBL: Y09392; CAA70561.1; -  
 DR EMBL: Y09392; CAA70559.1; -  
 DR EMBL: Y09392; CAA70560.1; -  
 DR EMBL: Y07263; AAC50819.1; -  
 DR EMBL: U83599; AAB41434.1; -  
 DR EMBL: U83600; AAB41435.1; -  
 DR EMBL: U78029; AAB40918.1; -  
 DR EMBL: U74611; AAB39714.1; -  
 DR EMBL: U94501; AAC51306.1; -  
 DR EMBL: U94504; AAC51309.1; -  
 DR EMBL: U94502; AAC51307.1; -  
 DR EMBL: U94503; AAC51308.1; -  
 DR EMBL: U94505; AAC51310.1; -  
 DR EMBL: U94506; AAC51311.1; -  
 DR EMBL: U94507; AAC51312.1; -  
 DR EMBL: U94508; AAC51313.1; -  
 DR EMBL: U94509; AAC51314.1; -  
 DR EMBL: U94510; AAC51315.1; -  
 DR EMBL: U94512; AAC51316.1; -  
 DR EMBL: U83598; AAB41433.1; -  
 DR EMBL: AF026070; AAC39356.1; -  
 DR EMBL: AF026071; AAB82288.1; -  
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 DR EMBL: AB051851; BAB40663.1; -  
 DR EMBL: U75380; AAC51192.1; -  
 DR EMBL: U75381; AAC51193.1; -  
 DR EMBL: U83597; AAB41432.1; -  
 DR Genew: HGNC:11910; TNFRSF25.  
 DR MIM: 603366; -  
 DR GO: GO:0005829; C:cytosol; NAS.  
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO: GO:0016329; F:apoptosis regulator activity; NAS.  
 DR GO: GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.

DR GO: GO:0004872; F:receptor activity; NAS.  
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . . ; TAS.  
 DR GO: GO:0008624; P:induction of apoptosis by extracellular sig. . . ; TAS.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_C6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_C6; 2.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 1.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 DR Repeat: Apoptosis; Transmembrane; Alternative splicing; Signal;  
 DR Repeat: Polymorphism.  
 FT SIGNAL 1 24  
 FT CHAIN 25 417  
 FT DOMAIN 25 199  
 FT TRANSMEM 200 220  
 FT DOMAIN 221 417  
 FT REPEAT 34 71  
 FT REPEAT 72 115  
 FT REPEAT 116 163  
 FT REPEAT 164 192  
 FT DOMAIN 332 413  
 FT DISULFID 35 47  
 Query Match 8.88; Score 191; DB 1; Length 417;  
 Best Local Similarity 22.98; Pred. No. 5.1e-07;  
 Matches 84; Conservative 46; Mismatches 155; Indels 82; Gaps 16;  
 QY 81 CPFGHISE-----DGRDCISCKYGOD---YSTMNDLLFLCRTRCD--SGEVELSP 128  
 DB 51 CPAGHYLKAPCTERPCGNSGTLCVCP--QDFLAWENHNHS--ECARQACDEQASVALEN 106  
 QY 129 CTTTRNTVCCCEESTFE-----ESPCKRC-----RFGCRGAKVGDCT 171  
 DB 107 CSAVADTRCCCKFEWFECVSOVSSSPYCPCLDGLAHRTRLLCSRRPTDGTCL 166  
 QY 172 PW-----SDIEYHKSSG-----IIGVVAAVLVAVFVCKSLMKK 210  
 DB 167 PGFEYHGDGCVSCTSTSLGSCPERCAVCGMRQMFVQVLVLAGVLPVLLGATLITYRH 226  
 QY 211 VLPYLGKICGGGGPERVDRSSORPGADNVLEIVLSILOPVPQDEMEVO-----E 264  
 DB 227 CWPBKPLVTADDEAG---MEALTPPATHTSLPSDASATTLAPDSSSEKICTVOVGVNSWT 282  
 QY 265 PAEPPTGVNMLSPGS-----EHLLEPAEASQRRLVLPANEDPTFLR---QCFD 314  
 DB 283 PGYPTQDALCPQVYVWSMDLPSRALGPAAP-----TSPESPAGSPAMVLPGPOLY- 336  
 QY 315 DFADLVFDSMEPLMRKLGIMDNEIKVAKAEAGHRDTLYTMLIKWNKTRGDSVHTLL 374  
 DB 337 DVMADVARRMKKEVRLGLREAEIENVEYIGRFROQYEMLKRW--RQOQFAGLGAVY 394  
 QY 375 DALETIG 381  
 DB 395 AALERMG 401  
 RESULT 12  
 TNFR\_HUMAN STANDARD; PRT; 335 AA.  
 AC P25445; Q14292; Q14293; Q14294; Q14295; Q16652;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).  
 GN TNFRSF6 OR APT1 OR FAS OR FASL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_Taxid=9606;



RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE-91309137; PubMed-1713127;  
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,  
RT Sameshima M., Hase A., Seto Y., Nagata S.;  
RT "The polypeptide encoded by the cDNA for human cell surface antigen  
RT Fas can mediate apoptosis.";  
RL Cell 66:233-243(1991).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND  
RP 321-335.  
RX MEDLINE-92268122; PubMed-1375228;  
RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,  
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,  
RA Krammer P.H.;  
RT "Purification and molecular cloning of the APO-1 cell surface  
RT antigen, a member of the tumor necrosis factor/nerve growth factor  
RT receptor superfamily. Sequence identity with the Fas antigen.";  
RL J. Biol. Chem. 267:10709-10715(1992).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION.  
RX MEDLINE-95181785; PubMed-7533181;  
RA Cascino I., Flucci G., Papoff G., Ruberti G.;  
RT "Three functional soluble forms of the human apoptosis-inducing Fas  
RT molecule are produced by alternative splicing.";  
RL J. Immunol. 154:2706-2713(1995).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 5).  
RX TISSUE-Peripheral blood lymphocytes;  
RA Schetzlein C.E., Poehlmann R., Philippson P., Eibel H.;  
RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).  
RX MEDLINE-96238926; PubMed-8648105;  
RA Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;  
RT "An N-terminal domain shared by Fas/Apo-1 (CD95) soluble variants  
RT prevents cell death in vitro.";  
RL J. Immunol. 156:4622-4630(1996).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX TISSUE-Urinary bladder;  
RA MEDLINE-22388257; PubMed-12477932;  
RA Klausberg R.L., Feinhold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Plange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,  
RT Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [7]  
RP INTERACTION WITH RIPK1.  
RX MEDLINE-95277838; PubMed-7538908;  
RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;  
RT "RIP, a novel protein containing a death domain that interacts with  
RT Fas/Apo-1 (CD95) in yeast and causes cell death.";  
RL Cell 81:513-523(1995).  
RN [8]  
RP STRUCTURE BY NMR OF 218-335.  
RX MEDLINE-97122332; PubMed-8967952;  
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;  
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";  
RL Nature 384:638-641(1996).  
RN [9]  
RP VARIANT ALPS PRO-241.  
RX MEDLINE-95300225; PubMed-7540117;  
RA Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A.,  
RA Lin A.Y., Strober W., Lenardo M.J., Puck J.M.;  
RT "Dominant interfering Fas gene mutations impair apoptosis in a human  
RT autoimmune lymphoproliferative syndrome.";  
RL Cell 81:935-946(1995).  
RN [10]  
RP VARIANT ALPS TYR-260.  
RX MEDLINE-97068823; PubMed-8929361;  
RA Drappa J., Valshteyn A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;  
RT "Fas gene mutations in the Canale-Smith syndrome, an inherited  
RT lymphoproliferative disorder associated with autoimmunity.";  
RL New Engl. J. Med. 335:1643-1649(1996).  
RN [11]  
RP VARIANT ALPS TRP-121 AND CYS-232.  
RX MEDLINE-97180145; PubMed-9028321;  
RA Bettinardi A., Brugnoni D., Quiros-Roldan E., Malagoli A.,  
RA laGutta S., Corrao A., Notarangelo L.D.;  
RT "Missense mutations in the Fas gene resulting in autoimmune  
RT lymphoproliferative syndrome: a molecular and immunological  
RT analysis.";  
RL Blood 89:902-909(1997).  
RN [12]  
RP VARIANT ALPS ASP-257 AND SER-310.  
RX MEDLINE-97180739; PubMed-9028957;  
RA Sneller M.C., Wang J., Dale J.K., Strober W., Middleton L.A., Choi Y.,  
RA Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,  
RA Straus S.E.;  
RT "Clincial, immunologic, and genetic features of an autoimmune  
RT lymphoproliferative syndrome associated with abnormal lymphocyte  
RT apoptosis.";  
RL Blood 89:1341-1348(1997).  
RN [13]  
RP VARIANT ALPS ALA-28.  
RX MEDLINE-97463833; PubMed-9322534;  
RA Pensati L., Costanzo A., Ianni A., Accapezzato D., Iorio R.,  
RA Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente A.,  
RA Leyre M.;  
RT "Fas/Apo1 mutations and autoimmune lymphoproliferative syndrome in a  
RT patient with type 2 autoimmune hepatitis.";  
RL Gastroenterology 113:1384-1389(1997).  
RN [14]  
RP VARIANT ALPS VAL-260.  
RX MEDLINE-99038860; PubMed-9821419;  
RA Infante A.J., Britton H.A., DenNapoli T., Middleton L.A., Lenardo M.J.,  
RA Jackson C.E., Wang J., Fleisher T., Straus S.E., Puck J.M.;  
RT "The clinical spectrum in a large kindred with autoimmune  
RT lymphoproliferative syndrome caused by a Fas mutation that impairs  
RT lymphocyte apoptosis.";  
RL J. Pediatr. 133:629-633(1998).  
RN [15]  
RP VARIANT ALPS LYS-241 AND GLN-250.  
RX MEDLINE-99192346; PubMed-10090885;  
RA Jackson C.E., Fischer R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J.,  
RA Dale J.K., Fleisher T.A., Middleton L.A., Sneller M.C., Lenardo M.J.,  
RA Straus S.E., Puck J.M.;  
RT "Autoimmune lymphoproliferative syndrome with defective Fas: genotype  
RT influences penetrance.";  
RL Am. J. Hum. Genet. 64:1002-1014(1999).  
RN [16]  
RP VARIANT ALPS GLY-272.  
RX MEDLINE-99270228; PubMed-10340403;  
RA Peters A.M., Kohlfink B., Martin H., Griesinger F., Worman B.,  
RA Gahr M., Roessler J.;  
RT "Defective apoptosis due to a point mutation in the death domain of  
RT CD95 associated with autoimmune lymphoproliferative syndrome, T-cell  
RT lymphoma, and Hodgkin's disease.";  
RL Exp. Hematol. 27:868-874(1999).  
RN [17]

RP VARIANTS ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.  
 RX MEDLINE-99126461; PubMed-9927496;  
 RA Vaisnaw A.K., Orlinick J.R., Chu J.-L., Krammer P.H., Chao M.V.,  
 RA Elkon K.B.;  
 RT "The molecular basis for apoptotic defects in patients with CD95  
 RT (Fas/Apo-1) mutations.";  
 RL J. Clin. Invest. 103:355-363(1999).  
 RN [18]  
 RP VARIANTS NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-183; ILE-198;  
 RP VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299.  
 RX MEDLINE-99003325; PubMed-9787134;  
 RA Groenbaek K., Straten P.T., Ralkjær E., Ahrenkiel V., Andersen M.K.,  
 RA Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.;  
 RT "Somatic Fas mutations in non-Hodgkin's lymphoma: association with  
 RT extranodal disease and autoimmunity.";  
 RL Blood 92:3018-3024(1998).  
 RN [19]  
 RP VARIANTS ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.  
 RX MEDLINE-21311411; PubMed-11418480;  
 RA Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,  
 RA Roosen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,  
 RA Fischer R.E., Jackson C.M., Lin A.Y., Baemler C., Siegfert E.,  
 RA Marx A., Vaisnaw A.K., Grodzicky T., Fleisher T.A., Leonardo M.J.;  
 RT "The development of lymphomas in families with autoimmune  
 RT lymphoproliferative syndrome with germline Fas mutations and  
 RT defective lymphocyte apoptosis.";  
 RL Blood 98:194-200(2001).  
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD  
 CC recruits caspase-8 to the activated receptor. The resulting death-  
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic  
 CC activation which initiates the subsequent cascade of caspases  
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-  
 CC mediated apoptosis may have a role in the induction of peripheral  
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or  
 CC both. The secreted isoforms 2 to 6 block apoptosis (in vitro).  
 CC -1- SUBUNIT: Binds DAXX (by similarity). Binds RIPK1.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);  
 CC secreted (isoforms 2 to 6).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=6;  
 CC Name=1;  
 CC  
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 Best Local Similarity 22.1%; Pred. No. 5.5e-07;  
 Matches 83; Conservative 63; Mismatches 131; Indels 106; Gaps 16;

RESULT 13  
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 AC P51867;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL  
 DE receptor) (Apoptosis-mediating surface antigen Fas) (Apo-1 antigen)  
 DE (CD95).  
 GN TNFSF6 OR APT1 OR FAS.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96226401; PubMed-8634151;  
 RA Yoo J., Stone R.T., Beattie C.W.;  
 RT "Cloning and characterization of the bovine Fas.";  
 RL DNA Cell Biol. 15:227-234(1996).  
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD  
 CC recruits caspase-8 to the activated receptor. The resulting death-  
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic  
 CC activation which initiates the subsequent cascade of caspases  
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-  
 CC mediated apoptosis may have a role in the induction of peripheral  
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or  
 CC both (by similarity).  
 CC -1- SUBUNIT: Binds DAXX and RIPK1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.  
 CC -1- SIMILARITY: Contains 1 death domain.  
 CC  
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 CC  
 DR EMBL: U34794; AAC48546.1; -;  
 DR HSSP; P25445; IDDF.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;  
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 FT CHAIN 17 323  
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 FT  
 FT DOMAIN 17 170  
 FT TNFRSEM 171 188  
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 FT DISULFID 82 98









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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:14:55 ; Search time 42 Seconds

(without alignments)  
941.079 Million cell updates/sec

Title: US-10-052-798-1

Perfect score: 2169

Sequence: 1 MEORCONAPASGARRKHP.....HLLSGKFMYLEGNADSAXS 411

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238.5	11.0	461	2 JC4302	tumor necrosis fac
2	210.5	9.7	455	1 GOMST1	tumor necrosis fac
3	209	9.6	454	1 GOMST1	tumor necrosis fac
4	192	8.9	327	2 A46484	apoptosis-mediati
5	189	8.7	335	2 A40036	tumor necrosis fac
6	179	8.3	435	2 I54182	tumor necrosis fac
7	175.5	8.1	461	1 GORTM1	tumor necrosis fac
8	173.5	8.0	314	2 I37383	FAS soluble protei
9	158	7.3	324	2 JC2395	Fas antigen precu
10	152	7.0	416	1 JN0006	nerve growth facto
11	151.5	7.0	461	1 A35356	tumor necrosis fac
12	142.5	6.6	425	1 A26431	nerve growth facto
13	142.5	6.6	427	1 GOMST1	hypothetical prote
14	141.5	6.5	348	2 T28623	gene murine tumou
15	139	6.4	459	2 I48854	gene G4R protein - vari
16	138.5	6.4	349	2 D72175	gene G4R protein - vari
17	138.5	6.4	349	2 D36858	gene G4R protein - vari
18	135	6.2	474	2 B36858	gene G4R protein - vari
19	133.5	6.2	271	2 SI2783	CD30 antigen precu
20	131.5	6.1	272	2 I48700	CD30 antigen precu
21	130	6.0	272	2 A60771	gene ox40 protein
22	122	5.6	326	1 GOMST1	T2 protein - myxom
23	122	5.6	326	1 GOMST1	T2 protein - myxom
24	120	5.6	326	1 GOMST1	T2 protein - myxom
25	118.5	5.5	1036	2 T25933	hypothetical prote
26	117	5.4	1036	2 T25933	scavenger receptor
27	114.5	5.3	651	2 JC7705	OX40 homolog - hum
28	114	5.3	305	2 A46476	death receptor - hum
29	113.5	5.2	256	2 B32393	B cell-associated T-cell antigen 4-1

30	113.5	5.2	1356	2 A45445	janusin precursor,
31	112.5	5.2	557	2 A48434	variant-specific s
32	112	5.2	1353	1 JH0675	restrictin precus
33	111.5	5.1	1810	1 A32230	tenascin precursor
34	110.5	5.1	962	2 JC5571	subtilisin-like pr
35	110.5	5.1	975	2 JC5570	serine proteinase
36	110.5	5.1	1548	2 S34583	T2 protein - rabbi
37	110	5.1	325	2 B43692	R-cadherin precus
38	108.5	5.0	913	1 A47543	probable regulator
39	108	5.0	1346	2 A57376	hypothetical prote
40	108	5.0	2824	2 T27259	myb-related protei
41	107.5	5.0	327	2 T01038	fertilin alpha-1
42	107.5	5.0	905	2 S55059	beta-lactamase (EC
43	106.5	4.9	2201	2 A32160	tenascin-C - human
44	106.5	4.9	2201	2 A32160	polyferredoxin 6x2
45	106	4.9	398	1 S24802	

## ALIGNMENTS

RESULT 1	
JC4302	tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)	
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999	
C:Accession: JC4302; PC4093	
R:Suter, B.; Pauli, U	
Gene 163, 263-266, 1995	
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.	
A:Reference number: JC4302; MUID:96011645; PMID:7590278	
A:Accession: JC4302	
A:Molecule type: mRNA	
A:Residues: 1-461 <SUT>	
A:Cross-references: GB:019994; NID:91141752; PIDN:AAC48499.1; PID:91141753	
A:Accession: PC4093	
A:Molecule type: protein	
A:Residues: 1-7 <SUT>	
A:Experimental source: kidney cell line 15	
C:Genetics:	
A:Gene: Unif	
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology	
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor	
F:1-29/Domain: signal sequence #status predicted <SIG>	
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>	
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>	
F:84-82/Domain: NGF receptor repeat homology <NGF>	
F:211-231/Domain: transmembrane #status predicted <TM>	
F:361-447/Domain: signal transduction #status predicted <ST>	
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted	
Query Match	11.0%; Score 238.5; DB 2; Length 461;
Best/Local Similarity	24.4%; Pred. No. 8.5e-10;
Matches 117; Conservative 58; Mismatches 164; Indels 141; Gaps 26;	
OY	30 PGLVAPKTVLVVAAYLVLLV---SAESALLTQOOLAPQGRAPQKRSPE-----GLC 81
DB	7 FGLLP-----LVRLALVDVYRAGVHGLVLRPGREKESLCPOGKYSHPNRSICCTKC 62
OY	82 PGRHSHSD-----GRDCISCKYGOQYSTHMDLFCILCTCRDS--GEVELSPCTTTR 133
DB	63 HKGTLYLHNDCLGPGIDTCRECDNG-FTTASBNHLTCLSSKRSMSQYIEISCTYDR 121
OY	134 NTVQCQCEGTFREDSPEM--CRKCRGCGPRGMVYKVGDCPTWSDIECVHKSGLII---- 187
DB	122 DTVGCGRKNQYRKYSSETLFOCLNCSL-CPNGFVQL-PCLEKQPTIC-NCHSGFELRDK 178
OY	188 -----GTVAAVYLI-----VAIVV-----CKSLW 208
DB	179 CVSGVNCNKADCKNLCPTATSETRNDPDTGTVLLPLVIFFGCLAFELVGLACRQWR 238
OY	209 KKVLPYKLGICSGGG-----GDPERVDRS-----SORPGAEDVNLNEIVSIL 250

Db 239 K---PKLYSIICGKSTPVKEDEPEPLATAPSFCDITTFSPISPSPTTFSPVSPSPIS 295  
251 QPTQV---EDMEVQEEPAE-----PTGVNMLSP-----GSEHLLERPEA 288  
Db 296 SPFTTCDMSNKTSPKKTAPPQAGPTLPMPAPSTVPYTPPLPKWGGSAHSAHSA 355  
QY 289 ERSQRRLVPAVNGDPTETLRQCFADLVFPDSNEPLRLKGLMDNEI-KYAKAEAA 347  
356 QLA-----DADA-TLYAVVDG---VPTTRKEFPARRGLSEHELERELONGR 400  
QY 348 GHRDTLYTMLIKVNNKGTG-RDASVH-----TLDAETLGERL---AKQIEDHL 394  
Db 401 CLREAQYSMLAEWRRRTSRREATLELLGSLVLRDMDLLGLCEDIEALRGARLAPAPHL 460

RESULT 2  
GQHOT1  
tumor necrosis factor receptor 1 precursor [validated] - human  
N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1  
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000  
C:Accession: A38208; A34899; A34900; A36555; A38281; S12057; J0758; A60231; A38  
R:Funcs: P.; Strehl, S.; Dworzak, M.; Hummler, A.; Ambros, P.F.  
A:Title: Structure of the human TNF receptor 1 (p50) gene (TNFR1) and localization to ch  
A:Reference number: A38208; MUID:92250049; PMID:1315717  
A:Accession: A38208  
A:Molecule type: DNA  
A:Residues: 1-455 <FUC>  
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:9339748; PIDN:AAA61201.1; PID:G  
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lessl  
Cell 61, 351-359, 1990  
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep  
A:Reference number: A34899; MUID:90235284; PMID:2158862  
A:Accession: A34899  
A:Molecule type: mRNA  
A:Residues: 1-455 <LOE>  
A:Cross-references: GB:M58286; GB:M34480; NID:9339753; PIDN:AAA6753.1; PID:9339754  
A:Experimental source: Placenta  
A:Note: Part of this sequence, including the amino end of the mature protein, confirmed  
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Galanaga, T.  
Cell 61, 361-370, 1990  
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor  
A:Reference number: A34900; MUID:90235285; PMID:2158863  
A:Accession: A34900  
A:Molecule type: mRNA  
A:Residues: 1-455 <SCH>  
A:Cross-references: GB:M33294; NID:9339744; PIDN:AAA03210.1; PID:9339745  
R:Hummler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;  
DNA Cell Biol. 9, 705-715, 1990  
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recept  
A:Reference number: A36555; MUID:91090841; PMID:1702293  
A:Accession: A36555  
A:Molecule type: mRNA  
A:Residues: 1-455 <HTM>  
A:Cross-references: GB:M63121; NID:9339755; PIDN:AAA6754.1; PID:9339756  
A:Accession: C36555  
A:Molecule type: protein  
A:Residues: 30-361-41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104, 107-128, 162-167, 'X', 169-2  
A:Note: The purified protein, called tumor necrosis factor binding protein, is a soluble  
R:Gay, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
A:Reference number: A38281; MUID:91017509; PMID:2170974  
A:Accession: A38281  
A:Molecule type: mRNA  
A:Residues: 1-455 <GRA>  
A:Cross-references: GB:M37764  
R:Koppar, Y.; Kemper, O.; Brakelbusch, C.; Engelmann, H.; Zwarg, R.; Aderka, D.; Holtmann  
EMBO J. 9, 3269-3278, 1990

A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the  
le form of the receptor.  
A:Reference number: S12057; MUID:91006021; PMID:1698610  
A:Accession: S12057  
A:Molecule type: mRNA  
A:Residues: 1-455 <NDP>  
A:Cross-references: EMBL:X55313; NID:937223; PIDN:CAA39021.1; PID:937224  
A:Note: Parts of soluble TNF binding protein 1, including its amino and carboxyl ends  
R:Kemper, O.; Wallach, D.  
Gene 134, 209-216, 1993  
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor  
A:Reference number: J0758; MUID:94085779; PMID:8262379  
A:Accession: J0758  
A:Molecule type: DNA  
A:Residues: 1-13 <KEM>  
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
Eur. J. Immunol. 20, 1167-1174, 1990  
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequ  
A:Reference number: A60231; MUID:90292116; PMID:2113477  
A:Accession: A60231  
A:Molecule type: protein  
A:Residues: 41-43, 'X', 45-53, 'X', 55-57, <SEC>  
R:Galanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Luccl III, J.A.; Jeffes, E.W.B.;  
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis fa  
lients.  
A:Reference number: A38258; MUID:91062364; PMID:2174164  
A:Accession: A38258  
A:Molecule type: protein  
A:Residues: 41-60 <GAT>  
A:Experimental source: cancer patient serum  
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyrell, H.; Grubb, A.; Adolf, G.  
Eur. J. Haematol. 42, 270-275, 1989  
A:Title: Isolation and characterization of a tumor necrosis factor binding protein fr  
A:Reference number: A60594; MUID:89171156; PMID:2924890  
A:Accession: A60594  
A:Molecule type: protein  
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>  
A:Experimental source: renal failure patient urine  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden  
A:Reference number: A35010; MUID:90110215; PMID:2153136  
A:Accession: A35010  
A:Molecule type: protein  
A:Residues: 41-45 <ENG>  
A:Experimental source: normal urine  
R:Kajihara, J.; Asada, A.; Kiritahara, S.; Kato, K.  
Biocell. Biotechnol. Biochem. 58, 2266-2268, 1994  
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified  
A:Reference number: JC2404; MUID:95128033; PMID:7765720  
A:Accession: JC2404  
A:Molecule type: protein  
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>  
A:Experimental source: urine  
A:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)  
C:Genetics:  
A:Gene: GDB:TNFR1  
A:Cross-references: GDB:125913; OMIM:191190  
A:Map position: 12p13.2-12p13.2  
A:Intons: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-45/Domain: tumor necrosis factor receptor 1 #status predicted <MAT>  
F:30-211/Domain: extracellular #status predicted <EXT>  
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #stat  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-196/Domain: NGF receptor repeat homology <NG4>  
F:212-234/Domain: transmembrane #status predicted <MEM>  
F:235-455/Domain: intracellular #status predicted <INT>





Db 369 ARKKEFMFMGLSEHEIRLEMQNRCLEAQQYSMLFAMRRTPRHE-----DTLEVVG 422  
OY 382 ERLAKOKI 389  
Db 423 LVLSKMNLL 430

## RESULT 4

A:Accession: A46484  
A:Status: preliminary  
A:Molecule type: mRNA

A:Cross-references: GB:M33649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
A:Experimental source: BM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.

Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A:Title: Aberrant transcription caused by the insertion of an early transposable element

A:Reference number: A47254; MUID:91189576; PMID:7680478  
A:Accession: A47254

A:Status: preliminary  
A:Molecule type: nucleic acid

A:Cross-references: GB:M33649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
A:Experimental source: BM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.

Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A:Title: Aberrant transcription caused by the insertion of an early transposable element

A:Reference number: A47254; MUID:91189576; PMID:7680478  
A:Accession: A47254

A:Status: preliminary  
A:Molecule type: nucleic acid

A:Cross-references: GB:M33649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
A:Experimental source: BM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.

Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A:Title: Aberrant transcription caused by the insertion of an early transposable element

A:Reference number: A47254; MUID:91189576; PMID:7680478  
A:Accession: A47254

A:Status: preliminary  
A:Molecule type: nucleic acid

A:Cross-references: GB:M33649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
A:Experimental source: BM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.

Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A:Title: Aberrant transcription caused by the insertion of an early transposable element

A:Reference number: A47254; MUID:91189576; PMID:7680478  
A:Accession: A47254

A:Status: preliminary  
A:Molecule type: nucleic acid

A:Cross-references: GB:M33649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
A:Experimental source: BM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.

Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A:Title: Aberrant transcription caused by the insertion of an early transposable element

A:Reference number: A47254; MUID:91189576; PMID:7680478  
A:Accession: A47254

A:Status: preliminary  
A:Molecule type: nucleic acid

A:Cross-references: GB:M33649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
A:Experimental source: BM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.

Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A:Title: Aberrant transcription caused by the insertion of an early transposable element

A:Reference number: A47254; MUID:91189576; PMID:7680478  
A:Accession: A47254

A:Status: preliminary  
A:Molecule type: nucleic acid

A:Cross-references: GB:M33649; NID:g193225; PIDN:AAA37593.1; PID:g193226  
A:Experimental source: BM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.

Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A:Title: Aberrant transcription caused by the insertion of an early transposable element

A:Reference number: A47254; MUID:91189576; PMID:7680478  
A:Accession: A47254

A:Status: preliminary  
A:Molecule type: nucleic acid

N:Alternate names: surface antigen Apo-1

C:Species: Homo sapiens (man)

C:Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 21-Jul-2000

C:Accession: A40036; S24543; A38142

R:Ritch, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Ha

Cell 66, 233-243, 1991

A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can m

A:Reference number: A40036; MUID:91309137; PMID:1713127

A:Accession: A40036

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <ITD>

A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410

R:Krimmer, P.H.

submitted to the EMBL Data Library, February 1992

A:Reference number: S24543

A:Accession: S24543

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <KRA>

A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742

R:Roehm, A.; Behrmann, I.; Falk, W.; Pawlitta, M.; Maier, G.; Klas, C.; Li-Weber, M.; R

J. Biol. Chem. 267, 10709-10715, 1992

A:Title: Purification and molecular cloning of the Apo-1 cell surface antigen, a memb

A:Reference number: A38142; MUID:92268122; PMID:1375228

A:Accession: A38142

A:Status: preliminary, not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-134, 'Q', 136-335 <OE>

A:Experimental source: SKW6.4 cells

A:Note: sequence extracted from NCBI backbone (NCBIN:103810)

A:Note: In NCBI backbone the source is designated as mouse

C:Genetics: APT1

A:Gene: GDB:APT1

A:Cross-references: GDB:132671; OMIM:134637

A:Map position: 10q24.1-10q24.1

C:Superfamily: NGF receptor repeat homology

C:Keywords: apoptosis; surface antigen; transmembrane protein

F:1-16/Domain: signal sequence #status predicted <SIG>

F:85-128/Domain: NGF receptor repeat homology <NG4>

F:174-190/Domain: transmembrane #status predicted <TM>

Query Match 8.9%, Score 192; DB 2; Length 327;  
Best Local Similarity 25.1%, Pred. No. 1.4e-06;  
Matches 82; Conservative 49; Mismatches 130; Indels 66; Gaps 17;

OY 38 LVLVAAVLLVLSAALITQODLAPQORAPQOKRSSPSEGL-----CPGHI 87

Db 8 LPLVLASQLRVHTQGNISISLSLKRKHVETDKNC--SEGLYQCGPCCOPCGKK 65

OY 88 SEDR-----DCISCKYGDY--STHNDLLFCLRCTRCDG---EVELSPCTTTRTV 136

Db 66 VEDCKNMGVPTCAPCTEGREYMDKNHYADK--CRRLDDEHGLEVEIN--CTLTQTK 122

OY 137 CCGCEGTFREDESPMKCRKTCGPRGNVAVGCTPMSDIECVKESGIIIVTAAVYL 196

Db 123 CKCRPDYCSGPCGHCVRC--ASCENHGLE--PCTASNTNCRKOSPRNRLMLTLIVLL 179

OY 197 IVAAFVC-----KSLMKKVLPLYLKIGSGGGGDEPERDRSSORGAEDNVNELVSILOP 252

Db 180 LPLVITRKIRKRCMKR-----RODDE--SRYSRTIPMNASNLSL----- 222

OY 253 TOVPE--QEMVQAPPTGVNMLSPGSEHLLPEAEASORR--RLTV-----PANEDP 305

Db 223 KYIRIADMTIQOAKKFAFARNNKEKGKIDIMHDSIODTAEOKVOLLICVYQSHGSDA 282

OY 306 TETL-----RQCFDDPADLVFPD 323

Db 283 YODLTKGLKKAECRRITLDFQDMVQKD 309

## RESULT 5

A40036  
apoptosis-mediating surface antigen Fas precursor - human

Query Match 8.7%, Score 189; DB 2; Length 335;  
Best Local Similarity 22.1%, Pred. No. 2.4e-06;  
Matches 85; Conservative 63; Mismatches 111; Indels 106; Gaps 16;

OY 38 LVLVAAVLLV-----VSAESALITQODLAPQORAPQOKRSSPSEGL-----CP 83

Db 8 LPLVLTSAVRLSSKSVNAOVTDINSKGL--ELRKTVTTFVETQNLGHHHGOFCCHKPCPP 65

OY 84 GHH-----ISEDRDCISCKYGDYSTHNDLLFCLRCTRCDG---EVELSPCTTTRN 134

Db 66 GERKARDCVNGDPPDCVPCQEGKEVYDKAFSSKRCRCRCDGEGHGLEVEIN--CTATQN 124

OY 135 TVCCGEGTFREDESPMKCRKTCGPRGNVAVGCTPMSDIECVKESGIIIVTAAVYL 194

Db 125 TKCRKKNFNCNSVCHDPC--TKCHGIIK--ECLTISNTKKEGSSNLSL----- 175

OY 195 VLIIVAVCKSLMKKVLPLYLKIGSGGGGDEPERVDSORPGAEDNVNELVSILOPQ 254

Db 176 -----WLCILLPLIPLIWVK-----RKEVQKTCRKHREKNGSHS-----SPTL 215

OY 255 VPQEMVQAPPTGVNMLSPGSEHLLPEAEASORRRLVLANEGPTEITLRCCFD 314

Db 216 NP-----ETVAINLSDVDLSKYI-----T 234

OY 315 DFADLVFDSWEPILMKIGLMDNEIKVAKAAGHRDTL--YTMILKVNKTGRDASVH 371

Db 235 TIAGVNTLSQYKGVKRVKNGV--NEAKIDEIKNDNVDTAEOKVOLLKNNHQLHGKKEAYD 292

OY 372 TLIDALE-----TLGERLAROKIED 391

Db 293 TLIKDKKANICITLAKIOTIILKD 317

## RESULT 6

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)  
C:Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 17-Mar-2000

C:Accession: I54182

R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.  
Genomics 16, 214-218, 1993

A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen

A:Reference number: I54182; MUID:93252381; PMID:8486360

A:Accession: I54182

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-435 &lt;RES&gt;

A:Cross-references: GB:I04270; NID:9339761; PIDN:AAA6757.1; PID:9339762

C:Genetics:

A:Gene: GDB:LTBR

A:Cross-references: GDB:1230195; OMIM:600979

A:Map position: 12p13.3-12p13.1

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 8.3%; Score 179; DB 2; Length 435;

Best Local Similarity 24.7%; Pred. No. 1.7e-05;

Matches 72; Conservative 28; Mismatches 91; Indels 100; Gaps 15;

81 CRRGHHSDD---RD--CISCKGODYSTHNDLFLCLRCTRD--SGEVELSPCTTR 133

62 CRRGHHSDD---RD--CISCKGODYSTHNDLFLCLRCTRD--SGEVELSPCTTR 120

134 NTVCOCSEGTFR---EDSP-----EMCRKCRG----- 159

121 KQCGCQCPGEMFCAAMALECTHCELLSDCPRTGAELEKDEYKGNHCVCKKQHNTSS 180

160 -----CP-RGKAVKVDCTPMSDIECVH-----KESGIIIGVTV---AAVLI 197

181 PSARCOPHTRCENOGILEAPGTAOSDTTCKNPLLEPLPEMGTMMLVLLPLAFELL 240

198 VAVFCKSLTK-----KVLPLYKGTICSGGGGDEPERDRSSQPRGADNVLEIVSL 250

241 ATVFSC---TWKSHPSLCKLGLSLKRRPQSGPNNV---AGSWEPKAKHYPPDLVPL 294

251 OPTQ-----VPEQEMEVQEPAPPTGVNMLSPGSEHL 282

295 LPTSDVSPVSTGLPAAPVLEAGVPQ-----QSPDLDTREQLPEQSQV 341

Db

RESULT 7

GORRT1

tumor necrosis factor receptor 1 precursor - rat

N:Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 22-Jun-1999

C:Accession: B36555

R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantze, M.;  
DNA Cell Biol. 9, 705-715, 1990

A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto

A:Reference number: A36555; MUID:91090841; PMID:1702293

A:Accession: B36555

A:Molecule type: mRNA

A:Residues: 1-461 &lt;HIM&gt;

A:Cross-references: GB:M63122; NID:9207361; PIDN:AAA42256.1; PID:9207362

C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-23/Domain: signal sequence #status predicted &lt;SIG&gt;

F:30-61/Product: tumor necrosis factor receptor type 1 #status predicted &lt;MAT&gt;

F:30-21/Domain: extracellular #status predicted &lt;EXT&gt;

F:30-201/Product: tumor necrosis factor binding protein #status predicted &lt;BTP&gt;

F:4-82/Domain: NGF receptor repeat homology &lt;NG1&gt;

F:84-126/Domain: NGF receptor repeat homology &lt;NG2&gt;

F:127-167/Domain: NGF receptor repeat homology &lt;NG3&gt;

F:168-204/Domain: NGF receptor repeat homology &lt;NG4&gt;

F:212-234/Domain: transmembrane #status predicted &lt;MTM&gt;

F:235-461/Domain: intracellular #status predicted &lt;INT&gt;

F:54,151,201/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 8.1%; Score 175.5; DB 1; Length 461;

Best Local Similarity 21.6%; Pred. No. 3.3e-05;

Matches 104; Conservative 58; Mismatches 153; Indels 167; Gaps 25;

30 PCLRPKTLVVAVALLV---SASALI-TQODLAPQGRAPQGRSSPSG-----LC 81

7 PCL---LTLVLALMLGTHPSGYGLVPSLGRKRNILCPQGYAHAKNNSICCTKC 62

82 PRGHHSDD---GRD--CISCKGODYSTHNDLFLCLRCTRC--DSGEVELSPCTTR 133

63 HKGYLVSDCPSRPGQETVEYCDKG-TTASQNHVROGLSCCTCKREMQVIEISCKADM 121

134 NTVCOCSEGTFR---EDSPKCRKCRGCPGMKV-----GDCT 171

122 DTVCGCKKNQFOFVYLETHTFQCVDG-SPCFNGTVTLPCKEKONTVCNCHAGFELSGNECT 180

172 PMS---DIECVH-----KESGIIIGVTVAAVY-LIVAVFCKSL-----WK 209

181 PSCHCKKNOCKMLCLPVAANTNPQDSTAVLLPLVFLGLCLFFICTISLCRYPM- 239

210 KVLPLYKGTICSGGGGDEPERDRSSQPRGADNVLEIVSLPTQVPEQEME-----VQBP 265

240 -----RP-----RVYIITGRDSAPKVEGEGVTKRP 266

266 AEPGVNMLSPG-----SEHLEPAEARSOR-----RLVPAVE 302

267 LTPASIPAPSPNGFNPRTLGFSTPRFSHPVSTPISPVFGSPNMHNPVPRVREVPQ 326

303 GPR-----TETLQCCFDPA-----DLVPDSMEPLMRKG 333

327 ADPLYGSLNPVPIPAVPRKMDVVAAPQRLDTADPAMLVAVVQGVPRTRKKEFRLLG 386

334 LMDNEI-KVAKAEAGHRTLTYLILKVNKTGR-----DASVHFLD-----ALETGE 382

387 LSEHETRELQNGRLRLRAHNSMLEAMRRRTPRHATIDVVGRYLCDNMLGCELEINE 446

383 RL 384

447 TL 448

Db

RESULT 8

I37383

FAS soluble protein - human

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jul-2000

C:Accession: I37383

R:Casano, I.; Flucel, G.; Papoff, G.; Rubertl, G.  
J. Immunol. 154, 2706-2713, 1995

A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule

A:Reference number: I37383; MUID:95181785; PMID:7533181

A:Accession: I37383

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-314 &lt;RES&gt;

A:Cross-references: EMBL:Z47993; NID:9728578; PIDN:CAA8031.1; PID:9695539

Query Match 8.0%; Score 173.5; DB 2; Length 314;

Best Local Similarity 31.1%; Pred. No. 3e-05;

Matches 51; Conservative 25; Mismatches 59; Indels 29; Gaps 8;

38 LVLVAAVALL-----VSASALITQODLAPQGRAPQGRSSPSG-----CPP 83

8 LPLVLTVARLSKSVNAQVTDINSKGL--ELRKTVTVETQNLBGLHHDGQFCRKP 65

84 GHH-----ISDGRICSGKGYSTHNDLFLCLRCTRDSG---EVELSPCTTTRN 134

66 GERKARDCTVNGDEPDCVPCQEGKEYTDKRAHSSKCRRLCDGGLVEITN-CTR 124

OY 135 TVOCSEGTFFREDSPEMCKRKTGCPRCWVKVGDCTPMEDIC 178  
 125 TKRCCKPNEFCNSTVCEHCDCP-TKCEHGIK--ECTLISNTKC 165

## RESULT 9

Fas antigen precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 20-Feb-1995 #sequence, revision 20-Feb-1995 #text, change 05-Nov-1999  
 C:Accession: J03295; PC2246  
 R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.,  
 Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
 A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver  
 A:Reference number: J03295; M01D:94128114; PMID:7507668

A:Accession: J03295  
 A:Molecule type: mRNA  
 A:Residues: 1-324 <KIM>  
 A:Cross-references: DDBJ:D26112; NID:9468486; PIDN:BA05108.1; PID:d1005650; PID:9468487  
 A:Experimental source: thymus  
 A:Accession: PC2246  
 A:Molecule type: mRNA  
 A:Residues: 1-62, 'RPT' <K12>  
 A:Cross-references: DDBJ:D26113; NID:9468488; PIDN:BA05109.1; PID:d1005651; PID:9468489  
 A:Experimental source: liver  
 C:Genetics:  
 A:Introns: 62/1  
 C:Superfamily: NGF receptor repeat homology  
 C:Keywords: transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-324/Product: Fas antigen #status predicted <MAT>  
 F:4-79/Domain: NGF receptor repeat homology <NGF>  
 F:81-124/Domain: NGF receptor repeat homology <NGF>  
 F:171-188/Domain: transmembrane #status predicted <TM>

Query Match 7.3%; Score 158; DB 2; Length 324;  
 Best Local Similarity 28.1%; Pred. No. 0.00041;  
 Matches 66; Conservative 33; Mismatches 84; Indels 52; Gaps 14;

OY 39 VLVAAVLLVSAESALITQDLPAPQRAAPQOKRS-----SPSGL-----CP 82  
 1 MLTIMVLLPLVLAPELNVRMGTDSIFEGLELKRVSRETNNCSGELYQVGFCCQPC 60  
 DB 83 PGHISED-----GRDCISCKYGDYS--THMNDLFLCRTCPSG--EVELSPCT 131  
 61 PGRKAKDCCTSGCATCPCTGEGEYTRKHKHSDK--CRKAFCEGHLEVEFTN-CTR 117  
 OY 132 TRNTVCCCEBGTFFREDSPEMCKRKTGCPRCWVKVGD-CTPWSDIECVHKESGI-IIGV 189  
 118 TONTKCRCKENFCNALSIDHCYHC-TSC--GLEDLLEPCTRTSNTRCKKSSNYKLML 174  
 DB 190 TVAAVLLVAVFVCKSLMKKVLPLYLKGICSGGGPDERDRSSQPRGADNVLN 244  
 175 LILGLALILFVFLYKR--YRKRP-----GDE-----SGIPSPSPVMN 212

## RESULT 10

JN0006  
 N:Alternate names: NGF receptor, low affinity precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 10-Sep-1999  
 C:Accession: JN0006; A60504  
 R:Large, T.H.; Meskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid  
 Neuron 2, 1133-1134, 1989  
 A:Title: Structure and developmental expression of the nerve growth factor receptor in t  
 A:Reference number: JN0006; M01D:9016579; PMID:2560385

A:Accession: JN0006  
 A:Molecule type: mRNA  
 A:Residues: 1-416 <LAR>  
 A:Experimental source: embryonic chick brain  
 R:Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.

Dev. Biol. 137, 287-304, 1990

A:Title: Structure and developmental expression of the chicken NGF receptor.  
 A:Reference number: A60504; M01D:90152140; PMID:2154393  
 A:Accession: A60504  
 A:Molecule type: mRNA  
 A:Status: preliminary; not compared with conceptual translation  
 A:Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom  
 C:Comment: The cysteine-rich region of the extracellular domain may form part of all  
 C:Comment: This protein is thought to form a high-affinity receptor when it associate  
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C:Keywords: duplication; signal sequence #status predicted <SIG>  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-416/Product: nerve growth factor receptor #status predicted <MAT>  
 F:21-239/Domain: extracellular #status predicted <EXT>  
 F:24-57/Domain: NGF receptor repeat homology <NG1>  
 F:59-100/Domain: NGF receptor repeat homology <NG2>  
 F:101-139/Domain: NGF receptor repeat homology <NG3>  
 F:141-181/Domain: NGF receptor repeat homology <NG4>  
 F:189-237/Region: serine/threonine-rich  
 F:240-261/Domain: transmembrane #status predicted <MEM>  
 F:262-416/Domain: intracellular #status predicted <INT>  
 F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 152; DB 1; Length 416;  
 Best Local Similarity 21.9%; Pred. No. 0.0015;  
 Matches 88; Conservative 42; Mismatches 136; Indels 136; Gaps 21;

OY 81 CPP-----GHH-----ISEDGRDCISCKYGDYTHMNDL--FCLRCTDCSGEVELS 127  
 75 CKPCTOCVGLHSMAPCVESDDAVC--RCAYG-----YFODELSGSCKECSICEVGFGLMF 128  
 DB 128 PCTTNTVVC-OCEBGTFFREDSPEMCKRKTGCPRCWVKVGDCTPMEDIC--VHKES 183  
 129 PCNDSQDYCEBEPBETFSDEANFVDPCLPC-TICENENYMKCATATDABACRDLHPR- 186  
 OY 184 GIITGVAAVLLVAVFVCKSLMKKVLPLYLKGICSGGGPDERYDR----- 231  
 187 -----WTHHPSTL-----ASDSEPITRDPFNTGEMATTL 217  
 DB 232 -----SSQRP-----GADNVLNLTIVSLDPTQV-----PEQEM 260  
 218 ADIVTTVMGSSQPVSRGTADNLIPIYCSILAAVVGLVAYAFKRWNSCKONKOGANNR 277  
 DB 261 EVOEPAEPGVNMLSPG-----ESEHLEPAEAERSORRLIYVANEQDPT----- 306  
 278 PVNQTSPSECKEKLHSDSVDSQSLHDQPPNQSTQG---PAFGDGSILASLPSPSQ 333  
 DB 307 ETLRQCFDDFADLVPPDSWEPPIRLKGLMDNEIKVAKAAGHRTLYTMLIKVNRKTR 366  
 334 EYERKLLSSSAE-----ETWRQLAGELGYKEDLIDCTRESPAR-----ALLDW----- 379  
 OY 367 DASVHTLLDALLETLESLAKOKIEDHLLSSGKMYLEGANDS 408  
 380 SAKETATLDALLVALRKRIORGDAIESL-----YESSTATS 414  
 DB

## RESULT 11

A35356  
 N:Alternate names: factor receptor 2 precursor [validated] - human  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 08-Dec-2000  
 C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094  
 R:Smith, C.A.; Davis, T.; Anderson, D.; Sojlam, L.; Beckmann, M.P.; Jerzy, R.; Dower,  
 Science 248, 1019-1023, 1990  
 A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a  
 A:Reference number: A35356; M01D:90260639; PMID:2160731

A:Accession: A35356  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <SMI>  
 A:Cross-references: GB:M32315; NID:9189185; PIDN:AAA59929.1; PID:9189186

R.Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, P. *Proc. Natl. Acad. Sci. U.S.A.* 87, 8331-8335, 1990

ATitle: A second tumor necrosis factor receptor gene product can shed a naturally occurring soluble form

A:Reference number: A36475; MUID:91045991; PMID:2172983

A:Accession: A36475

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-195, 'R', 197-461 <KOH>

A:Cross-references: GB:M5594; GB:M38549; NID:9339757; PIDN:AAA36755.1; PID:9339758

R.Dembich, Z.; Loeschner, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. *Cytokine* 2, 231-237, 1990

ATitle: Two human TNF receptors have similar extracellular, but distinct intracellular, cytoplasmic tails

A:Reference number: A48416; MUID:91370690; PMID:1966549

A:Accession: A48416

A:Status: preliminary

A:Molecule type: protein

A:Residues: 23-461 <DM>

A:Cross-references: GB:S63368; NID:9235648; PIDN:AAH19824.1; PID:9235649

A>Note: sequence extracted from NCBI database (NCBI:65366, NCBI:65371)

R.Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. *Proc. Natl. Acad. Sci. U.S.A.* 87, 6151-6155, 1990

ATitle: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of its expression in human monocytes

A:Reference number: A36007; MUID:90349572; PMID:2166946

A:Accession: A36007

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>

A:Cross-references: GB:M5857; NID:9339751; PIDN:AAA6362.1; PID:9339752

R.Loetscher, H.; Schlegel, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. *J. Biol. Chem.* 265, 20131-20138, 1990

ATitle: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors

A:Reference number: A23666; MUID:91056048; PMID:2173696

A:Accession: A23666

A:Status: preliminary

A:Molecule type: protein

A:Residues: 23-40; 65-69; 136-141; 300-306 <OE>

R.Engelmann, H.; Novick, D.; Wallach, D. *J. Biol. Chem.* 265, 1531-1536, 1990

ATitle: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct receptors

A:Reference number: A35010; MUID:90110215; PMID:2155136

A:Accession: A35010

A:Status: preliminary

A:Molecule type: protein

A:Residues: 27-31 <ENG>

R.Kuhnert, P.; Kemper, O.; Wallach, D. *Gene* 150, 381-386, 1994

ATitle: Cloning, sequencing and partial functional characterization of the 5' region of the human TNF receptor

A:Reference number: I38094; MUID:95121934; PMID:7821811

A:Accession: I38094

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-37 <RES>

A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701

C.Genetics:

A:Gene: GDB:TNFR2

A:Cross-references: GDB:125914; OMIM:191191

A:Map position: 1p36.2-1p36.2

A:Introns: 26/3

A>Note: the list of introns is incomplete

C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F.1-22/Domains: signal sequence #status predicted <SIG>

F.23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>

F.40-76/Domains: NGF receptor repeat homology <NG1>

F.78-119/Domains: NGF receptor repeat homology <NG2>

F.120-162/Domains: NGF receptor repeat homology <NG3>

F.164-201/Domains: NGF receptor repeat homology <NG4>

F.262-279/Domains: transmembrane #status predicted <TMN>

F.280-461/Domains: intracellular #status predicted <INT>

F.171.193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 151.5; DB 1; Length 461;

Best Local Similarity 26.8%; Pred. No. 0.0018;

**Matches**: 63; Conservative: 19; Mismatches: 86; Indels: 67; Gaps: 14;

OY CPPEGH-----ISDEGRDCISKYGQDYSHWMDLFLCLRC-TRCDSEVLESPCTTNN 134  
|||  
Db CSPGHAHKVECTKTSDFVCSCE--DSTYTOLMNVNPPCLSCGSKSDDOETACTREON 115  
  
OY TVCCCGEGTEFEEDSPEMC-----RKCRTCPGPWGKKVDPCPWSINIECVHKESSGIIG 188  
:|||:::  
Db RICTCRPGWCALSKQBECRLCAPLRKRCKREF--GVAKPKC--TETSVPVKPCAPGTFSN 171  
  
OY VTVA-----VLIVAV-----FVCSSLMKKVLPYLKGICSGGGGDPERVRSSQ 234  
|||  
Db TTSTDTCRPHQIGNVVALIENMASMAVCHST-----SPRR----SM 209  
  
OY RPGEADVNLNEVISLIPTOVPOBOEME-VQEPAEPTGVMLSLP-GSESHILLEPAE 287  
|||  
Db APGA-----VHLPPVSTRSOHTOPTREPSTAFSTSFLLPWGPS---PPAE 252  
  
**RESULT**  
12  
A26431  
nerve growth factor receptor precursor, low affinity - rat  
N.Alternate names: NGF receptor  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
CAccession: A26431; PH1229  
R.Radeke, M.J.; Msisko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
Nature 325, 593-597, 1987  
A.Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.  
A.Reference number: A26431; PMID:87115859; PMID:3027580  
A.Accession: A26431  
A.Molecule type: mRNA  
A.Residues: 1-425 <RAD>  
A.Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756  
R.Meitsis, M.; Timmusk, T.; Allikmeets, R.; Saarma, M.; Persson, H.  
Gene 121, 247-254, 1992  
A>Title: Regulatory elements and transcriptional regulation by testosterone and retinoid  
A.Reference number: PH1229; PMID:93077038; PMID:1446821  
A.Accession: PH1229  
A.Molecule type: DNA  
A.Residues: 1-20 <MET>  
A.Cross-references: GB:X61269  
C.Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
C.Comment: The cysteine-rich region of the extracellular domain may form part or all  
C.Comment: This protein is thought to form a high-affinity receptor when it associates  
C.Genetics:  
A.Introns: 20/3  
C.Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C.Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptors  
F.1-29/Domain: signal sequence #status predicted <SIG>  
F.30-425/Product: nerve growth factor receptor #status predicted <ANT>  
F.30-251/Domain: extracellular #status predicted <EXT>  
F.33-66/Domain: NGF receptor repeat homology <NG1>  
F.68-109/Domain: NGF receptor repeat homology <NG2>  
F.110-148/Domain: NGF receptor repeat homology <NG3>  
F.150-190/Domain: NGF receptor repeat homology <NG4>  
F.198-249/Region: serine/threonine-rich  
F.252-273/Domain: transmembrane #status predicted <MEM>  
F.274-425/Domain: intracellular #status predicted <INT>  
F.61/Binding site: carbohydrate (Asn) (covalent) #status predicted

**Query Match:**            6.6%; Score 142.5; DB 1; Length 425;  
**Best Local Similarity:** 22.8%; Pred. No. 0.0075;  
**Matches**     87; Conservative: 38; Mismatches 142; Indels 115; Gaps 18;

OY QKRSSPSGLCPGHHISEDGRDCISKYG--QDYSHWMDLFLCLRCTRCDSEVELSP 128  
|||  
Db QSMSAP-----WEADDAVC-KRAYGYQDBERG-----HCAMCSVCEVGSLVS 138  
  
OY CTTRRNHYC-OCEGSTREE-DSEPDKRKCTGCPRGWKYKDCTPMSDIEC----- 178  
|||||  
OY CODOMNTCEBCEPBGTYSDEANHVDPCLP-C-TVEDTERLOCTTPPADACECIPIRWI 197  
|||

OY 179 -----VKESGIIIGVVAIVLIVAVFCKSLMKKVLPLYKGI 218  
 DB 198 PRSTPEGSSTAPSTOPEPEPQDLPVS--TVADMVTVM----- 237  
 OY 219 CSGGGGPERVDRSSQRGAGDNVINEIVSILOPTQVP-----EQEMEQEPAP 268  
 DB 238 ----GSSOPVYTR-----GTTDMILPYVCSILAAVVGVLVAVIAKRWNSCKONKOGANS 288  
 OY 269 TGVNMLSPGESEHIL-----LEPAEERSQRRLLVPAVEGDP-----ETLRQCF 313  
 DB 289 RPNVOTPEPEGEKILHSDGISVDSGLHDQOTHTQTASGQALKGCGNLYSSLPILTKR--- 345  
 OY 314 DDFADLVFPDSMEPLMKRLGLMDEIKYAKAPAGHRDTLYTMLIKWNTKGRDASVHTL 373  
 DB 346 EEVKLLNGDYTRHLAGELGYOPEHIDSFTHACPV-----ATLASW-----GAODSAT 395  
 OY 374 LDALETGERLAKOKIEDHLLS 395  
 DB 396 LDALLALRRIORADIYVESLCS 417

## RESULT 13

GONUN

nerve growth factor receptor precursor, low affinity [validated] - human  
 N:Alternate names: NGF receptor  
 C:Species: Homo sapiens (man)  
 C>Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 08-Dec-2000  
 C:Accession: A25218; A60204; S21689; I57638  
 R:Johnson, D.; Lananhan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.  
 Cell 47, 545-554, 1986  
 A>Title: Expression and structure of the human NGF receptor.  
 A:Reference number: A25218; MUID:87051725; PMID:3029337  
 A:Accession: A25218  
 A:Molecule type: mRNA  
 A:Residues: 1-427 <JOH>

A:CROSS-references: GB:M14764; NID:g189204; PIDN:AAA59544.1; PID:g189205  
 R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schaltechan, G.; Thompson, S.; Grob, P.;  
 J. Neurochem. 48, 225-232, 1987  
 A>Title: Purification and amino terminal sequencing of human melanoma nerve growth factor  
 A:Reference number: A60204; MUID:87085574; PMID:3025363  
 A:Accession: A60204  
 A:Molecule type: protein  
 A:Residues: 29-31, 'T', 33-42, 'T', 45-46, 'T', 50-51, 'X', 54-56 <MAR>  
 A:Experimental source: melanoma cell line A875  
 A>Note: this sequence has been corrected by a note added in proof to follow the nucleot  
 R:Visavayaajhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.  
 Arch. Biochem. Biophys. 294, 244-252, 1992  
 A>Title: Structural domains of the extracellular domain of human nerve growth factor rec  
 A:Reference number: S21689; MUID:92198017; PMID:1372492  
 A:Accession: S21689  
 A>Status: Preliminary  
 A:Molecule type: protein  
 A:Residues: 183-208 <VIS>  
 R:Sehgal, A.; Patil, N.; Chao, M.  
 Mol. Cell. Biol. 8, 3160-3167, 1988  
 A>Title: A constitutive promoter directs expression of the nerve growth factor receptor  
 A:Reference number: I57638; MUID:89096903; PMID:2850481  
 A:Accession: I57638  
 A>Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-22 <RES>  
 A:CROSS-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
 C:Comment: The cytosine-rich region of the extracellular domain may form part of all of  
 C:Comment: This receptor undergoes both N- and O-linked glycosylation.

C:Genetics:  
 A:Gene: GDB:NGFR  
 A:CROSS-references: GDB:I20234; OMIM:162010  
 A:Map position: 17q21-17q22  
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
 F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-427/Product: nerve growth factor receptor #status experimental <MAR>  
 F:29-250/Domain: extracellular #status predicted <EXT>  
 F:32-65/Domain: NGF receptor repeat homology <NG1>  
 F:67-108/Domain: NGF receptor repeat homology <NG2>  
 F:109-147/Domain: NGF receptor repeat homology <NG3>  
 F:149-189/Domain: NGF receptor repeat homology <NG4>  
 F:197-248/Region: serine/threonine-rich  
 F:251-272/Domain: transmembrane #status predicted <TRM>  
 F:273-427/Domain: intracellular #status predicted <INT>  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.6%; Score 142.5; DB 1; Length 427;  
 Best Local Similarity 20.0%; Pred. No. 0.0075;  
 Matches 86; Conservative 44; Mismatches 143; Indels 157; Gaps 17;

OY 81 CPGGHTSEDRDISCKYGDY-----SYNMNLLF-----CLRCRCD 120  
 DB 32 CPTGLY-THSGECKACNLGEGVAPCGANOTVCEPCLDSVTSDDVVSATPECKPCTECV 90  
 OY 121 SGEVELSPCTTTRNTVCCCEGTFREEDSP--EMCRKCRG-----CP 161  
 DB 91 GLQSMACVCEADAVCAAYGYODETGTGCEACRCEAGSLVFSQDKONTVCECP 150  
 OY 162 RGMV-----KVQDCTPMSDIECVH----- 180  
 DB 151 DGTYSDEANHYDPLCTVCEDETERQLRECTRMADAECEIPIGRWITRSTPEGSSTAP 210  
 OY 181 -----KESGIIIGVVAIVLV-----AVFCKSLMKKVLPLYKGI 218  
 DB 211 STQEPAPPEODLLASTVAGVYTTVMSSQPVTRGTTDLIPYCSILAAVVGVLAVYI 270  
 OY 219 C-----SCGGGPERVDRSSQRPAGEDVNLNEIVSILOPTQVPEQEMEQEPAP 267  
 DB 271 AFKRWNSCKONKOGANSRP-----VNQTPPEGEKILHSDSL-----SVDSGLHDQPT 321  
 OY 268 PT--GVNMLSPGESEHILPEAEERSQRRLLVPAVEGDPETLRQCFDFADLVPPDSW 325  
 DB 322 QTASGOALKGGGGYSSLPAPKREVER--LLNGSAG-----DTW 359  
 OY 326 EPLRKILGMONEIKVAKAEAGHRDTLYTMLIKWNTKGRDASVHTLDALETGERLA 385  
 DB 360 RHLGELGYOPEHIDSFTHACPV-----ATLASW--TQDSATLDALLAHL-----RRIQ 409  
 OY 386 KOKIEDHLLS 395  
 DB 410 RADLVESLCS 419

## RESULT 14

T28623

hypothetical protein G2R - variola major virus  
 C:Species: variola major virus  
 C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
 C:Accession: T28623  
 R:Masung, R.F.; Esposito, J.J.; Liu, L.T.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au  
 Nature 366, 748-751, 1993  
 A>Title: Potential virulence determinants in terminal regions of variola smallpox vir  
 A:Reference number: Z20488; MUID:94088747; PMID:8264798  
 A:Accession: T28623  
 A>Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-348 <MAS>  
 A:CROSS-references: EMBL:I2579; NID:g623595; PIDN:AAA60933.1; PID:g439102  
 A:Experimental source: strain Bangladesh 1975  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 6.5%; Score 141.5; DB 2; Length 348;  
 Best Local Similarity 29.4%; Pred. No. 0.0071;  
 Matches 42; Conservative 17; Mismatches 57; Indels 27; Gaps 8;

OY 53 SALTQODLAPQQAQKRRSPSEC-----LCPGHHHT-----SEDRGDCISCKY 99  
 DB 13 SCIIINGDAAY--TPPNCKCKDTEYKRHNHLCCLSCPGTYASRLCDSTNTDCCPCGS 69







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:07:40 ; Search time 86 Seconds  
(without alignments)  
758.565 Million cell updates/sec

Title: US-10-052-798-1

Perfect score: 2169  
Sequence: 1 MGRGNAPADAGARRKRRP.....HLISGKFWYLRGNADSAAXS 411

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
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5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2167	99.9	411	19	AAW79261
2	2167	99.9	411	20	AAW88410
3	2167	99.9	411	20	AAW83321
4	2167	99.9	411	21	AAW55805
5	2167	99.9	411	22	AAU04038
6	2167	99.9	411	22	AAW73442
7	2167	99.9	411	22	AAW73443
8	2167	99.9	411	23	ABG31490
9	2167	99.9	411	23	AAW51080

10	2167	99.9	411	23	AAU76947	Human Apo2 protein
11	2167	99.9	411	23	ABW09602	Amino acid sequenc
12	2167	99.9	411	24	ABG75645	Human Tango-63e pr
13	2167	99.9	411	24	ABG74383	Human TNFR family
14	2163	99.7	411	20	AAW93576	Human hAP08 protei
15	2163	99.7	411	20	AAW00932	Human DR5 protein
16	2160	99.6	411	19	AAW79083	Human death domain
17	2160	99.6	411	20	AAW93608	Human killer adria
18	2160	99.6	411	21	ABE29790	Human death domain
19	2160	99.6	411	24	ABG71903	Human TRAIL recept
20	2160	99.6	411	24	ABU03488	Angiogenesis-assoc
21	2152	99.2	411	19	AAW76827	Human TR6 protein.
22	2152	99.2	411	22	AAW48348	Human tumour necro
23	2142.5	98.8	440	19	AAW92260	Tumour necrosis fa
24	2138.5	98.6	440	20	AAW05725	Tumour necrosis fa
25	2138.5	98.6	440	21	AAW01340	TNF-related apopto
26	2138.5	98.6	440	23	ABG62170	Human prostate spe
27	2135.5	98.5	440	19	AAW9284	Human TRAIL recept
28	2135.5	98.5	440	23	AAW51079	Human DR5 receptor
29	2133.5	98.4	440	24	ABG75644	Human Tango-63d pr
30	1610.5	74.3	350	20	AAW00934	Human DR5 protein
31	1597	73.6	303	19	AAW76828	Human TR6 partial
32	1597	73.6	303	22	AAW48349	Partial amino acid
33	1072	49.4	410	20	AAW93577	Human APOB protein
34	1072	49.4	468	19	AAW64483	Human DR4 protein.
35	1072	49.4	468	20	AAW31602	Human death recept
36	1072	49.4	468	20	AAW93609	Human DR4 protein.
37	1072	49.4	468	21	AAW72022	Human Death Domain
38	1072	49.4	468	21	AAW08546	Amino acid sequenc
39	1072	49.4	468	21	AAW01339	TNF-related apopto
40	1072	49.4	468	22	AAW49241	Human DR4 receptor
41	1072	49.4	468	23	AAW51078	Human DR4 receptor
42	1072	49.4	468	23	AAW75063	Human TNF related
43	1072	49.4	468	24	ABG71901	Human TRAIL recept
44	1070	49.3	468	21	AAW72023	Human Death Domain
45	1065	49.1	418	23	ABG31491	Human Apo-2Dcr ass

#### ALIGNMENTS

RESULT 1	AAW79261	standard; Protein: 411 AA.
ID	AAW79261	
AC	AAW79261	
XX		
DT	15-FEB-1999	(first entry)
XX		
DE	Tumour necrosis factor receptor related protein Tango-63e.	
XX		
KW	Tango-63e: tumour necrosis factor receptor related protein; human;	
KW	apoptosis; cancer; autoimmune disease; neurodegenerative disease.	
XX		
OS	Homo sapiens.	
XX		
PN	W09846643-A1.	
XX		
PD	22-OCT-1998.	
XX		
PF	16-APR-1998;	98MO-US07694.
XX		
PR	16-APR-1997;	97US-0843652.
XX		
PA	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.	
XX		
PI	Holtzman D;	
XX		
DR	WPI: 1998-594562/50.	
XX		
PT	Isolated tumour necrosis factor related proteins - used to develop products for the diagnosis and treatment of apoptosis-related	



Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORGONAPASGARRKHGPGPREARGARGLVPTLVVVAVALLVSAESALITQOD 60  
DB 1 MEORGONAPASGARRKHGPGPREARGARGLVPTLVVVAVALLVSAESALITQOD 60  
QY 61 LAPQORAAPOQRKSSPSEGLCPGHHISEDRDCISCKYGQDYSTMNDLFLCRLCTCD 120  
DB 61 LAPQORAAPOQRKSSPSEGLCPGHHISEDRDCISCKYGQDYSTMNDLFLCRLCTCD 120  
QY 121 SGVEVLSPTCTTNTNYCQCEEGTFREDDSPEMCRKCTCGPRGMVVGDCPTMSDIECVH 180  
DB 121 SGVEVLSPTCTTNTNYCQCEEGTFREDDSPEMCRKCTCGPRGMVVGDCPTMSDIECVH 180  
QY 181 KESGIIIGTVAAVVLIVAVFVCKSLMKKVLPLYLGICSGGGGDDERVDSSQRGAED 240  
DB 181 KESGIIIGTVAAVVLIVAVFVCKSLMKKVLPLYLGICSGGGGDDERVDSSQRGAED 240  
QY 241 NVLNEIVSILQPTQVPEQEMEVQEPAPTCGVNMLSGESEHLLLEPAEAERSQRRLVPA 300  
DB 241 NVLNEIVSILQPTQVPEQEMEVQEPAPTCGVNMLSGESEHLLLEPAEAERSQRRLVPA 300  
QY 301 NEGDPTETLRQCFDDADLVFPDSWEPMLMKKGLMONEIKVAKAEAGHRDTLYTMLIKW 360  
DB 301 NEGDPTETLRQCFDDADLVFPDSWEPMLMKKGLMONEIKVAKAEAGHRDTLYTMLIKW 360  
QY 361 VNKTGRDASVHTLLDLALETGERLAKOKIEDHLLSGKFMYLEGNDASAXS 411  
DB 361 VNKTGRDASVHTLLDLALETGERLAKOKIEDHLLSGKFMYLEGNDASAXS 411

RESULT 3  
AAW83321  
ID AAW83321 standard; Protein: 411 AA.  
AC AAW83321;  
DT 16-MAR-1999 (first entry)  
XX  
DE Human Apo-2 protein.  
XX  
KW Human: Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
KW TNF cytokine.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT misc-difference 410  
FT /label= unknown  
FT /note= "encoded by WTS"  
XX  
XX WO9851793-A1.  
XX  
XX 19-NOV-1998.  
XX  
XX 14-MAY-1998; 98MO-US09704.  
XX  
XX 09-FEB-1998; 98US-0020746.  
XX 15-MAY-1997; 97US-0857216.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;  
XX  
XX WPI; 1999-045228/04.  
XX  
XX N-PSDB; AAV72526.  
XX  
XX Human Apo-2 polypeptide inducing apoptosis - useful to treat  
XX conditions linked with decreased apoptosis e.g. cancer, and produce  
XX antibodies to increase or decrease apoptosis  
XX  
XX Claim 1; Fig 1; 134pp; English.

XX  
CC The present sequence represents human Apo-2. Apo-2 can be used  
CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
CC to treat conditions associated with decreased apoptosis e.g. cancer.  
CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor  
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
CC can be used to identify agents activating Apo-2, useful to treat  
CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
CC therapeutically (e.g. those containing immunoglobulin sequences can be  
CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
CC antibodies). It can be used to produce antibodies which can be combined  
CC with a (particularly pharmacologically acceptable) carrier in compositions  
CC or used to produce dimeric molecules (especially homodimeric molecules  
CC comprising first and second Apo-2 antibodies). Agonistic (especially  
CC single-chain) antibodies can be administered to induce apoptosis in  
CC mammalian cancer cells, and antagonistic antibodies used to block  
CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
CC antibodies may also be used diagnostically e.g. to detect Apo-2  
CC expression in cells/tissues and in Apo-2 purification.

XX  
SQ Sequence 411 AA:  
Query Match 99.9%; Score 2167; DB 20; Length 411;  
Best local Similarity 100.0%; Pred. No. 3.3e-178;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORGONAPASGARRKHGPGPREARGARGLVPTLVVVAVALLVSAESALITQOD 60  
DB 1 MEORGONAPASGARRKHGPGPREARGARGLVPTLVVVAVALLVSAESALITQOD 60  
QY 61 LAPQORAAPOQRKSSPSEGLCPGHHISEDRDCISCKYGQDYSTMNDLFLCRLCTCD 120  
DB 61 LAPQORAAPOQRKSSPSEGLCPGHHISEDRDCISCKYGQDYSTMNDLFLCRLCTCD 120  
QY 121 SGVEVLSPTCTTNTNYCQCEEGTFREDDSPEMCRKCTCGPRGMVVGDCPTMSDIECVH 180  
DB 121 SGVEVLSPTCTTNTNYCQCEEGTFREDDSPEMCRKCTCGPRGMVVGDCPTMSDIECVH 180  
QY 181 KESGIIIGTVAAVVLIVAVFVCKSLMKKVLPLYLGICSGGGGDDERVDSSQRGAED 240  
DB 181 KESGIIIGTVAAVVLIVAVFVCKSLMKKVLPLYLGICSGGGGDDERVDSSQRGAED 240  
QY 241 NVLNEIVSILQPTQVPEQEMEVQEPAPTCGVNMLSGESEHLLLEPAEAERSQRRLVPA 300  
DB 241 NVLNEIVSILQPTQVPEQEMEVQEPAPTCGVNMLSGESEHLLLEPAEAERSQRRLVPA 300  
QY 301 NEGDPTETLRQCFDDADLVFPDSWEPMLMKKGLMONEIKVAKAEAGHRDTLYTMLIKW 360  
DB 301 NEGDPTETLRQCFDDADLVFPDSWEPMLMKKGLMONEIKVAKAEAGHRDTLYTMLIKW 360  
QY 361 VNKTGRDASVHTLLDLALETGERLAKOKIEDHLLSGKFMYLEGNDASAXS 411  
DB 361 VNKTGRDASVHTLLDLALETGERLAKOKIEDHLLSGKFMYLEGNDASAXS 411

RESULT 4  
AAV55805  
ID AAV55805 standard; Protein: 411 AA.  
AC AAV55805;  
DT 29-FEB-2000 (first entry)  
XX  
XX Human Apo-2 polypeptide.  
XX  
XX Apo-2 polypeptide; immunization; antigen; polyclonal antibody; cancer;  
XX monoclonal antibody; Apo-2L receptor; therapy; apoptosis; autoimmune;  
XX immune-mediated cell death; neurodegenerative; inflammatory.  
XX  
XX Homo sapiens.  
XX  
XX

Key	Location/Qualifiers
Misc-difference 410	/Label= unknown
FT	/note= "encoded by WNG"
PN	WO9964461-A2.
PN	16-DEC-1999.
PD	10-JUN-1999; 99WO-US13197.
PF	12-JUN-1998; 98US-0096637.
PR	(GEPH ) GENENTECH INC.
PA	Ashkenazi AJ, Chuntharapai A, Kim KJ;
PI	WPI; 2000-097520/08.
DR	N-PSDB; AA239630.
XX	
PT	Preparation of antibodies using 2 or more different antigens, used for
PT	producing antibodies against Apo-2 ligand receptors useful for inducing
XX	apoptosis, particularly in cancer cells
XX	
PS	Disclosure; Fig 5; 57pp; English.
XX	
CC	The invention provides a method for producing antibodies (Abs) by
CC	immunizing an animal with at least two different antigens. The method
CC	comprises: (a) immunizing an animal with at least two different antigens,
CC	to generate polyclonal Abs against each antigen in the animal; (b)
CC	preparing monoclonal Abs (MAbs) using immune cells of the above animal;
CC	and(c) screening the MAbs to identify one or more MAbs which bind to each
CC	antigen. The Abs obtained are Apo-2L receptor (antagonists and can be
CC	used for therapy. The Apo-2L receptor Abs can be used for enhancing
CC	immune-mediated cell death in cells expressing Apo-2L receptors.
CC	Agonistic Abs which specifically cross-react with 2 or more different
CC	Apo-2L receptors can be used for inducing apoptosis in mammalian cancer
CC	cells. Antagonistic Abs can be used for blocking apoptosis, e.g. in
CC	neurodegenerative disease, or to block potential autoimmune/inflammatory
CC	effects of Apo-2 resulting from NF-approx.kB activation. The Abs can also
CC	be used for detection, diagnosis and affinity purification. The method
CC	can reduce the number of animals that need to be immunized and sacrificed
CC	in order to make 2 or more MAbs with differing antigen-binding
CC	specificities. The present sequence represents a human Apo-2 polypeptide.
XX	
50	Sequence 411 AA:
Query Match	99.9%; Score 2167; DB 21; Length 411;
Best Local Similarity	100.0%; Pred. NO. 3.3e-178;
Matches 411;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MEORGONPAASGARRKRGPPREARGARPGLVKTVLVYAAVLIVSASALITQOD 60
DB	1 MEORGONPAASGARRKRGPPREARGARPGLVKTVLVYAAVLIVSASALITQOD 60
QY	61 LAPQOARAPQOKRSSPSEGLCPRGHHSIEDGRDCTICKYGDYSTHMDLLFCLRCTGCD 120
DB	61 LAPQOARAPQOKRSSPSEGLCPRGHHSIEDGRDCTICKYGDYSTHMDLLFCLRCTGCD 120
QY	121 SGEVELSCTTTRNTVCCCEGTREEDSPEMCRKCRGCGRGMYKVGDCITPWSIDECVH 180
DB	121 SGEVELSCTTTRNTVCCCEGTREEDSPEMCRKCRGCGRGMYKVGDCITPWSIDECVH 180
QY	181 KESGIIGVYAAAVLIYAVFVCSLSLKKKLYLPYLGKIGSGGGGPERVNDSSORPGAED 240
DB	181 KESGIIGVYAAAVLIYAVFVCSLSLKKKLYLPYLGKIGSGGGGPERVNDSSORPGAED 240
QY	241 NVLNEIYSIIPTQVPEQEMEYQEAEDPTGVNMLSPGSEHLLPEPAEERSQRRLLVPA 300
DB	241 NVLNEIYSIIPTQVPEQEMEYQEAEDPTGVNMLSPGSEHLLPEPAEERSQRRLLVPA 300
QY	301 NEGSPTEILRCGFDFADLVFPDSNEPLMKRLGLMDNETIKYAKAPAAAGHRTLYMLIKW 360
DB	301 NEGSPTEILRCGFDFADLVFPDSNEPLMKRLGLMDNETIKYAKAPAAAGHRTLYMLIKW 360

Db	301	MEGDPETTLAQCHDDPFDADLVPEPDSWEPMLRKRLGLMDNETKAKAAFAAACHRDTLYTMLIKW	360
Oy	361	VNKTGRDASVHTLLDLALETGERLAKQKIEDHLLSSGKFMYLEGNADSAXS	411
Db	361	VNKTGRDASVHTLLDLALETGERLAKQKIEDHLLSSGKFMYLEGNADSAXS	411
RESULT 5			
AAU04038			
ID	AAU04038	standard; Protein; 411 AA.	
XX			
AC	AAU04038;		
XX			
DT	23-OCT-2001	(first entry)	
XX			
DE	Human apoptotic protein, Apo-2.		
XX			
KV	Human: Apo-2; Apo-2L receptor; immunogen; monoclonal antibody;		
KW	Cancer; tumour; apoptosis; lymphoma; Diastoma; sarcoma; leukemia;		
KM	3H3.14.5.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 410	/label= OTHER	
FT		/note= "Other= Leu or Met"	
PN	US6252050-B1.		
XX			
PD	26-JUN-2001.		
XX			
PF	10-JUN-1999;	99US-0329633.	
XX			
PR	12-JUN-1998;	98US-0089253.	
XX			
PA	(GETH ) GENENTECH INC.		
XX			
PI	Ashkenazi AJ, Chuntharapai A, Kim KJ;		
XX			
DR	WPI: 2001-424490/45.		
XX	N-PSDB: AAS07626.		
XX			
PT	Novel human monoclonal antibody for inducing apoptosis in mammalian		
PT	cancer cells; specifically cross-reacts with two or more different		
PT	Apo-2 ligand receptors		
XX			
PS	Example 1; Fig 5; 29pp; English.		
XX			
CC	The sequence represents human Apo-2, an apoptotic protein used as an		
CC	immunogen to make the monoclonal antibodies of the invention. The		
CC	invention relates to an isolated antibody which specifically cross-reacts		
CC	with two or more different Apo-2 ligand (Apo-2L) receptors. Apoptosis by		
CC	monoclonal antibody 3H3.14.5 after crosslinking with anti-mouse Ig was		
CC	tested. Human 9D cells in complete RPMI medium were added. Cells were		
CC	incubated with the monoclonal antibody in 100 micro on ice for 15		
CC	minutes. Cells were then incubated with goat anti-mouse IgG Fc complete		
CC	RPMI medium overnight at 37 degrees C. After washing once with PBS, cells		
CC	were resuspended in PBS containing 0.5% BSA and incubated with FITC-		
CC	Annexin and propidium iodide for 15 minutes in the dark. Dead cells were		
CC	detected by FACSscan. The 3H3.14.5 antibody was able to inhibit apoptosis		
CC	induced by interaction between Apo-2L and Apo-2. This antibody was		
CC	further capable of inducing apoptosis of 9D cells in the presence of an		
CC	anti-Fc antibody to cross-link antibodies. The antibodies are useful for		
CC	inducing apoptosis in mammalian cancer cells for treating cancer		
CC	including carcinoma, lymphoma, blastoma, sarcoma and leukemia, and are		
CC	useful in diagnostic assays for their antigen, e.g. detecting its		
CC	expression in specific cells, tissues or serum and for affinity		
CC	purification of antigen from recombinant cell culture or natural sources.		
XX			
Sequence	411 AA;		
50			

Best Local Similarity 100.0%; Pred. No. 3.3e-178;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MEORGONAPASGARRKHGPGPREARARGRLVPTLVVAVALLVSAESALITQOD 60
DB 1 MEORGONAPASGARRKHGPGPREARARGRLVPTLVVAVALLVSAESALITQOD 60
OY 61 LAPQORAAPOOKRSSPSEGICPPGHNTSEGRDICSCKYGQDYSTHNDLLFCRLCTRC 120
DB 61 LAPQORAAPOOKRSSPSEGICPPGHNTSEGRDICSCKYGQDYSTHNDLLFCRLCTRC 120
OY 121 SGEVELSPCTTTRNTVQCCEGTFREEDSPDMCKRCRTGCPGMVKGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVQCCEGTFREEDSPDMCKRCRTGCPGMVKGDCTPMSDIECVH 180
OY 181 KESGIITGVAAVAVLVAVFVCKSLMKVLPYLKICGGGGDPRVRSSQRRPAED 240
DB 181 KESGIITGVAAVAVLVAVFVCKSLMKVLPYLKICGGGGDPRVRSSQRRPAED 240
OY 241 NVLNEIVSILOPTQVPEQEMEVOPAPRTGVNMLSPSEHLLPEPAERSQRRRLVPA 300
DB 241 NVLNEIVSILOPTQVPEQEMEVOPAPRTGVNMLSPSEHLLPEPAERSQRRRLVPA 300
OY 301 NEGDPTETLRQCEDDFADLVFPDSWEPLMKRLGIMDNEIKVAAEAAGHDITLYTMLIKW 360
DB 301 NEGDPTETLRQCEDDFADLVFPDSWEPLMKRLGIMDNEIKVAAEAAGHDITLYTMLIKW 360
OY 361 VNKTRGRASVHTLLDALETGGERLAKOKIEDHLLSSKRFMYLDEGNADSAXS 411
DB 361 VNKTRGRASVHTLLDALETGGERLAKOKIEDHLLSSKRFMYLDEGNADSAXS 411

```

```

RESULT 6
AAB73442
ID AAB73442 standard; Protein: 411 AA.
XX
AC AAB73442:
XX
DT 25-JUN-2001 (first entry)
DE Human Apo-2 receptor precursor, SEQ ID NO:2.
XX
KW Human Apo-2 receptor; caspase-dependent apoptosis induction;
  programmed cell death; pro-apoptotic; death domain;
  agonistic antibody; nuclear factor kappa B;
  NF-kappa-B activation; cancer; tumour; lung cancer;
  colon cancer; glioma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..53
FT Protein /note= "Signal peptide"
FT /note= "Mature human Apo-2 receptor"
FT Domain 54..182
FT /note= "Extracellular domain. This domain is
  alternatively residues 1-182, or residues 1-130"
FT Disulfide-bond 81..94
FT Domain 96..137
FT /note= "Cysteine-rich pseudorepeat domain #1"
FT Disulfide-bond 97..113
FT Binding-site 106
FT /note= "Binds Apo-2L"
FT Binding-site 112
FT /note= "Binds Apo-2L"
FT Disulfide-bond 116..129
FT Disulfide-bond 119..137
FT Domain 138..183
FT /note= "Cysteine-rich pseudorepeat domain #2"
FT Disulfide-bond 139..153
FT Disulfide-bond 156..170
FT Disulfide-bond 160..178

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```

FT Domain 183..208
FT /note= "Transmembrane domain"
FT Domain 209..411
FT /note= "Intracellular domain"
FT Domain 324..391
FT /note= "Death domain"
FT Misc-difference 410
FT /label= Met, Leu
FT /note= "Encoded by WTG. This residue is Met in kidney
  Apo-2, and is Leu in pancreatic Apo-2"
XX
XX WO200119861-A2.
XX
XX 22-MAR-2001.
XX
XX 14-SEP-2000; 2000WO-US25436.
XX
XX 15-SEP-1999; 99US-0396710.
XX
XX (GETH ) GENENTECH INC.
XX
XX PI Ashkenazi AJ, Chuntherapai A, Kim KJ;
XX
XX DR WPI: 2001-266005/27.
XX
XX N-PSDB: AAF84481.
XX
XX PT Inducing apoptosis in mammalian cells for treating cancer, comprises
  exposing mammalian cells or cancer cells expressing Apo-2 receptor, to
  Apo-2 agonist antibody.
XX
XX PS Example 1; Fig 1; 90pp; English.
XX

```

```

CC The invention relates to a method for inducing apoptosis in mammalian
  cells which express the Apo-2 receptor protein (AAB73442, AAB73443).
CC The method involves exposing the cells to an Apo-2 agonistic antibody,
  which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor
  (also referred to simply as Apo-2) is a member of the tumour
  necrosis factor receptor (TNFR) family, and its natural ligand is the
  Apo-2 ligand (Apo-2L, also known as TRAIL). The Apo-2 receptor is able
  to trigger caspase-dependent apoptosis, and is also able to activate
  NF-kappa-B (nuclear factor kappa B). The Apo-2 receptor is an
  approximately 45 kD type I transmembrane protein, and contains a death
  domain in the cytoplasmic region (residues 324-392). It exhibits
  significantly more sequence identity to the apoptosis-linked receptor
  DR4, which also binds Apo-2L, than other apoptosis-associated proteins.
CC The Apo-2 receptor agonist monoclonal antibodies used in the method of
  the invention are 3F11.39.7, 3H3.14, 5, 305.1.10 and 3H1.18.10. The
  method of the invention is used to induce apoptosis in Apo-2-expressing
  cells, particularly cancer cells. It may therefore be used for treating
  CC mammalian cancers, especially lung cancer, colon cancer and glioma.
CC The present sequence represents human Apo-2 as encoded by cDNA isolated
  in an exemplification of the invention.
CC Note: The present sequence differs from the human Apo-2 receptor
  CC precursor given in AAB73443 in that residue 410 of this sequence can be
  Met or Leu, rather than Leu.
XX
XX SQ Sequence 411 AA:
XX
XX Query Match 99.9%; Score 2167; DB 22; Length 411;
  Best Local Similarity 100.0%; Pred. No. 3.3e-178;
  Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MEORGONAPASGARRKHGPGPREARARGRLVPTLVVAVALLVSAESALITQOD 60
DB 1 MEORGONAPASGARRKHGPGPREARARGRLVPTLVVAVALLVSAESALITQOD 60
OY 61 LAPQORAAPOOKRSSPSEGICPPGHNTSEGRDICSCKYGQDYSTHNDLLFCRLCTRC 120
DB 61 LAPQORAAPOOKRSSPSEGICPPGHNTSEGRDICSCKYGQDYSTHNDLLFCRLCTRC 120
OY 121 SGEVELSPCTTTRNTVQCCEGTFREEDSPDMCKRCRTGCPGMVKGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVQCCEGTFREEDSPDMCKRCRTGCPGMVKGDCTPMSDIECVH 180

```

QY	18	KESSIIIGVAAVAVLIVAAFEVCKSLIMKKVLPYLKIGTSGGGGPPERDRSSQRPAGD	24
DB	181	KESIIIGVAAVAVLIVAAFEVCKSLIMKKVLPYLKIGTSGGGGPPERDRSSQRPAGD	24
QY	241	NVLNEIYSIILOPTQVPEQEMEVQEPAPPTGVNMLSPGESEHLEPAEARSQRRLLVPA	30
DB	241	NVLNEIYSIILOPTQVPEQEMEVQEPAPPTGVNMLSPGESEHLEPAEARSQRRLLVPA	30
QY	301	NEGDPTETLQCCEDDFADLVPPFQSWEPRLKRLGLMDNEIKVAKAEAGHRDTLYTMLIKW	36
DB	301	NEGDPTETLQCCEDDFADLVPPFQSWEPRLKRLGLMDNEIKVAKAEAGHRDTLYTMLIKW	36
QY	361	VNKTGRPASVHTLLDALETIGEPLAKOKTIEDHLLSSGKFMVLEGNDASXIS	411
DB	361	VNKTGRPASVHTLLDALETIGEPLAKOKTIEDHLLSSGKFMVLEGNDASXIS	411
RESULT 7			
AC	AAB73443		
XX	AAB73443:		
XX	25-JUN-2001 (first entry)		
DE	Human Apo-2 receptor precursor, SEQ ID NO:6.		
XX			
KW	Human Apo-2 receptor; caspase-dependent apoptosis induction;		
KW	programmed cell death; pro-apoptotic; death domain;		
KW	agonistic antibody; nuclear factor kappa B;		
KW	NF-kappa-B activation; cancer; tumour; lung cancer;		
XX	colon cancer; glioma.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Peptide	1..53	
FT		/note= "Signal peptide"	
FT	Protein	54..411	
FT		/note= "Mature human Apo-2 receptor"	
FT	Domain	54..182	
FT		/note= "Extracellular domain. This domain is alternatively residues 1-182, or residues 1-130"	
FT	Disulfide-bond	81..94	
FT	Domain	96..137	
FT		/note= "Cysteine-rich pseudorepeat domain #1"	
FT	Disulfide-bond	97..113	
FT	Blinding-site	106	
FT		/note= "Binds Apo-2L"	
FT	Blinding-site	112	
FT		/note= "Binds Apo-2L"	
FT	Disulfide-bond	116..129	
FT	Disulfide-bond	118..137	
FT	Domain	138..183	
FT		/note= "Cysteine-rich pseudorepeat domain #2"	
FT	Disulfide-bond	139..153	
FT	Disulfide-bond	156..170	
FT	Disulfide-bond	160..178	
FT	Domain	183..208	
FT		/note= "Transmembrane domain"	
FT	Domain	209..411	
FT		/note= "Intracellular domain"	
FT	Domain	324..391	
FT		/note= "Death domain"	
FT	Misc-difference	410	
FT		/note= "Encoded by WTC"	
XX	WO200119861-A2.		
XX	22-MAR-2001.		
PE	14-SEP-2000; 2000WO-US25436.		

Pt		xx	15-SEP-1999;      99US-0396710.
Dx	(GETH ) GENENTECH INC.	xx PA	
DR	Ashkenazi AJ, Chuntherapai A, Kim KJ;	xx PI	
N-PSTDB:	AAAF84481.	xx DR	
WPI:	2001-266005/27.	xx Dd	
Inducing apoptosis in mammalian cells for treating cancer, comprises exposing mammalian cells or cancer cells expressing Apo-2 recomptress to Apo-2 agonist antibody -		PT Pt	
Example 1; Fig 2A; 90pp; English.		PS xx	
The invention relates to a method for inducing apoptosis in mammalian cells which expresses the Apo-2 receptor protein (AAF873442, AAF873443).		CC CC	
The method involves exposing the cells to an Apo-2 agonistic antibody,		CC CC	
which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor		CC CC	
(also referred to simply as Apo-2) is a member of the tumour		CC CC	
necrosis factor receptor (TNFR) family, and its natural ligand is the		CC CC	
Apo-2 ligand (Apo-2L, also known as TRAIL). The Apo-2 receptor is able		CC CC	
to trigger caspase-dependent apoptosis, and is also able to activate		CC CC	
NF-kappa-B (nuclear factor kappa B). The Apo-2 receptor is an		CC CC	
approximately 45 kD type I transmembrane protein, and contains a death		CC CC	
domain in the cytoplasmic region (residues 324-392). It exhibits		CC CC	
significantly more sequence identity to the apoptos-is-linked receptor		CC CC	
DR4, which also binds Apo-2L, than other apoptos-is-associated proteins.		CC CC	
The Apo-2 receptor against monoclonal antibodies used in the method of		CC CC	
the invention are 3F11.39.7, 3H3.14, 5, 3D5.1.10 and 3H1.18.10. The		CC CC	
method of the invention is used to induce apoptosis in Apo-2-expressing		CC CC	
cells, particularly cancer cells. It may therefore be used for treating		CC CC	
mammalian cancers, especially lung cancer, colon cancer and glioma.		CC CC	
Note: The present sequence represents human Apo-2 as given in figure 2A.		CC CC	
precursor given in AAB74442 in that residue 410 of this sequence is Leu,		CC CC	
rather than Met or Leu.		CC CC	
Sequence    411 AA:		SQ xx	
Query Match                 99.9%; Score 2167; DB 22; Length 411;			
Best Local Similarity          99.8% ; Pred. No. 3.3e+176;			
Matches    410; Conservative    0; Mismatches    1; Indels    0; Gaps    0;			
1 MEORGONAPASAGARKRHGPGRKRGARPGIGRVYKTIVLVVAALLVLSAESALITOOD 60	Oy		
I MEORRONPAPSAGAKRRHPGRPRKGARPGLVRPKTVTLVVAAALLVSASAALIITOD 60	Dd		
61 LAPOORAPPOQRSSSPSEGLCPRGNHIISEDRCISCKYGODYSHNMNLLFLCLCTRCTCD 120	Oy		
61 LAPOGARAPPOQRSSSPSEGLCPRGNHIISEDRCISCKYGGDYSHNMNDLFCLCRTCTCD 120	Dd		
121 SGEVELSFCYTTRNTVCOCCEGTREEDSDPEMKCRKRCTGCPRGMVKVGDCIPTSWSIDECVN 180	Oy		
121 SGEVELSCPCTTTRNTVMCCCEGTREFEEDSDPEMCKRCKRTGCCPRGMKVVDCTPWSDIECVH 180	Dd		
181 KESGIILGVTAAYVLVIYAIFVCSLSLMKKYLPLYLKIGICSGGGGPREVDNSOSQPGAEED 240	Oy		
181 KESGIILGVTAAYVLIYAIFVCSLSLMKKLYLPYLIKIGICSGGGGPREVDNSSSQPGAEED 240	Dd		
241 NVLNVEIVSILOPTYOVPEOEEMOVEFAEPBTGYNNMLSPGSEHNLEFPAAERSORRLPLPA 300	Oy		
241 NNLNEIVIISILOPTVPBDEMEVOFEAPEETGYNNMLS PGSEHNLBEPAEAERGORRLPLPA 300	Dd		
301 NEGDPTEELROCFDFADLVPFDSWEPMRKRLGLMDNEIKYAKAEAAGHRDTLYTMLIKW 360	Oy		
301 NEGDPTTELROCFDFADLVPFDSWEPMRMKLGLMDNEIKYAKAEAAGHRDTLYTMLIKW 360	Dd		
361 VNKKGRDAVSHTLLDALFTLGERRLKAOKRIEHILLSSGFMYLEGNAADSALS 411	Oy		
361 VNKTKGRDAVSHTLLDALFTTGERRLKAOKRIEHLISSGFMYLEGNAADSALS 411	Dd		

RESULT 8  
ABG31490  
ID ABG31490 standard; Protein: 411 AA.  
XX  
AC ABG31490;  
XX  
DT 21-NOV-2002 (first entry)  
XX  
DE Amino acid sequence for human Apo-2.  
XX  
KW Human; Apo-2Dcr; Apo-2 ligand; programmed cell death; apoptosis;  
KM neurodegenerative disease; autoimmune; inflammatory.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Misc-difference 410 /label= "Leu, Met  
FT /note= "Encoded by WTG"  
XX  
PN US2002102706-A1.  
XX  
PD 01-AUG-2002.  
PE 21-JUN-2001; 2001US-0887879.  
XX  
PR 18-JUN-1997; 97US-049911P.  
PR 12-JUN-1998; 98US-0096500.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Chantharapai A, Gurney A, Kim KJ, Wood WI;  
DR WPI: 2002-697823/75.  
DR N-PSDB; ABS53575.  
XX  
PT Novel isolated Apo-2Dcr polypeptide useful for modulating apoptosis in  
PT mammalian cells -  
XX  
PS Example 5; Fig 8; 58pp; English.  
XX  
CC The present invention relates to the isolation of novel human  
CC polypeptides, designated Apo-2Dcr, and the polynucleotide sequences  
CC encoding them. Apo-2Dcr is capable of binding Apo-2 ligand and is  
CC useful for modulating programmed cell death or apoptosis in  
CC mammalian cells. Apo-2Dcr can be used to produce apo-2Dcr antibodies  
CC which are useful therapeutically, and can cross-react with other  
CC receptors for Apo-2 ligand to block excessive apoptosis in  
CC neurodegenerative diseases, or to block potentially autoimmune  
CC or inflammatory effects. Apo-2Dcr antibodies are also useful in  
CC immunohistochemistry staining assays or diagnostic assays for  
CC Apo-2Dcr, e.g. detecting it's expression in specific cells, tissues  
CC or serum, and for the affinity purification of Apo-2Dcr from  
CC recombinant cell culture or natural sources. The present sequence  
CC represents human Apo-2.  
XX  
SQ Sequence 411 AA:  
Query Match 99.9%; Score 2167; DB 23; Length 411;  
Best Local Similarity 100.0%; Pred. No. 3.e-178;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MEORGNAPASGARRKRGPGRARGARGLRVPKTLVVAVALLVSAESALITQDD 60  
DB 1 MEORGNAPASGARRKRGPGRARGARGLRVPKTLVVAVALLVSAESALITQDD 60  
OY 61 LAPQORAPQOKRSSPEGLCPRGHNTSEGRDICTCKYGODVSTHNDLFLCRRCD 120  
DB 61 LAPQORAPQOKRSSPEGLCPRGHNTSEGRDICTCKYGODVSTHNDLFLCRRCD 120  
OY 121 SGEVELSPCTTTRNTVQCCEGTFRFEDSDPEMCKRCKTCGPRGNVKGDCPTWSDIECVH 180  
DB 121 SGEVELSPCTTTRNTVQCCEGTFRFEDSDPEMCKRCKTCGPRGNVKGDCPTWSDIECVH 180

DB 121 SGEVELSPCTTTRNTVQCCEGTFRFEDSDPEMCKRCKTCGPRGNVKGDCPTWSDIECVH 180  
OY 181 KESGIITGVAAVAVLVAAVFCVCKSLMKRVLPYKICGGGDDPERRVSSORPGEAD 240  
DB 181 KESGIITGVAAVAVLVAAVFCVCKSLMKRVLPYKICGGGDDPERRVSSORPGEAD 240  
OY 241 NVLNEIVSILOPTQVPEOMEVQEPAPPTGVNMLSPGESHLLEPAEFSQRRLVPA 300  
DB 241 NVLNEIVSILOPTQVPEOMEVQEPAPPTGVNMLSPGESHLLEPAEFSQRRLVPA 300  
OY 301 NEGDPTETLRQCEDEADLVPPDSWEPLMKRLGLMONEIVAKAAAGHRDTLYMLIKW 360  
DB 301 NEGDPTETLRQCEDEADLVPPDSWEPLMKRLGLMONEIVAKAAAGHRDTLYMLIKW 360  
OY 361 VNKTGRDASVHTLLDALETGERLAKKIDHLLSSKRYLGNMDSAXS 411  
DB 361 VNKTGRDASVHTLLDALETGERLAKKIDHLLSSKRYLGNMDSAXS 411  
RESULT 9  
AAM51080  
ID AAM51080 standard; Protein: 411 AA.  
XX  
AC AAM51080;  
XX  
DT 30-MAY-2002 (first entry)  
XX  
DE Human DR5 receptor.  
XX  
KM DR5 receptor; receptor; Apo-2 ligand; Apo-2L; agonist; human;  
KM apoptosis; colorectal cancer; tumour; antitumour; therapy.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Misc-difference 410 /note= "unidentified amino acid residue"  
FT  
XX  
PN W0200209755-A2.  
XX  
PD 07-FEB-2002.  
XX  
PE 27-JUL-2001; 2001WO-US23691.  
XX  
PR 27-JUL-2000; 2000US-221256P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Escandon E, Fox JA, Kelley SK, Xiang H;  
DR WPI: 2002-268997/31.  
XX  
XX  
PT Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I  
PT inhibitor class, and Apo-2 ligand receptor agonist for enhancing  
PT apoptosis in mammalian cells, or for treating cancer in a mammal  
XX  
PS Disclosure: Page 83-84; 84pp; English.  
XX  
CC The present sequence is that of human DR5 receptor, a receptor for  
CC Apo-2 ligand (Apo-2L). An alternative sequence for the D5 receptor  
CC is given in AAM51079. The invention relates to methods of inducing  
CC apoptosis in mammalian cells, and especially to the use of Apo-2L  
CC receptor agonists and CPT-11 (a chemotherapeutic agent of the  
CC topoisomerase I inhibitor class) to synergistically induce apoptosis  
CC in mammalian cells, in particular mammalian cancer cells, and  
CC especially colorectal cancer cells (claimed). The cells may be in  
CC cell culture or in a mammal, e.g. a mammal suffering from cancer or  
CC a condition in which induction of apoptosis in the cells is  
CC desirable. A claimed method of treating cancer in a mammal  
CC comprises administering CPT-11 and Apo-2L receptor agonist, where  
CC the CPT-11 is administered about 6-72 hours prior to administration  
CC of the Apo-2L receptor agonist. Preferred Apo-2L receptor agonists  
CC include Apo-2L and anti-DR4 or anti-DR5 receptor antibodies.



CC especially chimeric, humanised or human antibodies. Exposure of  
CC the cancer cells to CPT-11 and Apo-2L receptor agonist leads to  
CC upregulation of DR4 and DR5 receptors, directing the cells towards  
CC an apoptotic pathway rather than cell cycle arrest and possible DNA  
CC repair, thus providing enhanced antitumour activity.

XX Sequence 411 AA:

Query Match 99.9%; Score 2167; DB 23; Length 411;  
Best Local Similarity 100.0%; Pred. No. 3.3e-178;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEORQONAPASGARRHGPGRARGARPGRLRVKTLVLYVAALLVSAESALITQOD 60  
DB 1 MEORQONAPASGARRHGPGRARGARPGRLRVKTLVLYVAALLVSAESALITQOD 60  
OY 61 LAPQORAPQOKRSSPSGSLCPRGHHSDEGRDCISCKYGGDYSTHNDLLFCRLCTCD 120  
DB 61 LAPQORAPQOKRSSPSGSLCPRGHHSDEGRDCISCKYGGDYSTHNDLLFCRLCTCD 120  
OY 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMKCRKRTGCPRGVAVGDCIPMSDIECVH 180  
DB 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMKCRKRTGCPRGVAVGDCIPMSDIECVH 180  
OY 181 KESGIIIGVTAAVAVLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERVDSSORPGAED 240  
DB 181 KESGIIIGVTAAVAVLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERVDSSORPGAED 240  
OY 241 NVLNEIVSILOPTOVPEQEMEVQEPAPETGVNMLSPGSEHLLPEPAERQORRLVPA 300  
DB 241 NVLNEIVSILOPTOVPEQEMEVQEPAPETGVNMLSPGSEHLLPEPAERQORRLVPA 300  
OY 301 NEGPDETILROCFDFADLVFPDSMEPLMRKLGIMDNEIKAKAEAGHRDTLYTMLIKW 360  
DB 301 NEGPDETILROCFDFADLVFPDSMEPLMRKLGIMDNEIKAKAEAGHRDTLYTMLIKW 360  
OY 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
DB 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 10

AAU76947 standard; Protein: 411 AA.

AAU76947;

05-JUN-2002 (first entry)

Human Apo2 protein.

XX Apo-2; human; antibody; Apo-2L; cytostatic; neuroprotective;  
KW antiinflammatory; immunosuppressive; apoptosis; cancer;  
KW neurodegenerative disease; autoimmune disease; inflammatory disease.  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH Misc-difference 410  
FT /label- Ieu, Met  
FT /note- "This represents a naturally occurring  
variant of the apo-2 protein"

US2002004227-A1.

10-JAN-2002.

09-APR-2001; 2001US-0828739.

12-JUN-1998; 98US-089253P.  
10-JUN-1999; 99US-0329633.

PA (GETH ) GENE TECH INC.

XX Ashtkenazi AJ, Chuntharapai A, Kim KJ;  
PI WPI: 2002-239130/29.  
DR N-PSDB; ABR10298.

PT Novel nucleic acid encoding antibody that specifically cross-reacts  
PT with two or more different Apo-2 ligand receptors, useful for preparing  
PT the antibody by recombinant techniques  
PS Disclosure: Fig 5; 30pp: English.

XX This invention relates to an isolated nucleic acid comprising DNA  
CC encoding an antibody which specifically cross-reacts with two or more  
CC different Apo-2 and Apo-2L ligand (Apo-2L) receptors. The nucleotide  
CC sequences of the invention are useful for preparing anti-Apo2 antibodies  
CC by recombinant techniques, these antibodies may be employed to activate  
CC or stimulate apoptosis in cancer cells. The Apo-2L receptor antibodies  
CC are useful for enhancing immune-mediated cell death in cells expressing  
CC Apo-2L receptors. The antagonistic Apo-2L receptor antibodies may be  
CC used to block excessive apoptosis (neurodegenerative disease) or to  
CC block autoimmune/inflammatory effects of Apo-2 resulting from NFkBpAB  
CC activation. The antibodies encoded by the nucleotide sequences of the  
CC invention can also be used in diagnostic assays for their antigen e.g.,  
CC detecting its expression in specific cells, tissues or serum. The  
CC present sequence represents the human Apo-2 protein sequence used to  
CC generate anti-Apo-2 antibodies using the method of the invention. This  
CC sequence represents both naturally occurring natural variants of this  
CC cDNA ( Leucine or methionine at residue 410).

XX Sequence 411 AA:

Query Match 99.9%; Score 2167; DB 23; Length 411;  
Best Local Similarity 100.0%; Pred. No. 3.3e-178;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEORQONAPASGARRHGPGRARGARPGRLRVKTLVLYVAALLVSAESALITQOD 60  
DB 1 MEORQONAPASGARRHGPGRARGARPGRLRVKTLVLYVAALLVSAESALITQOD 60  
OY 61 LAPQORAPQOKRSSPSGSLCPRGHHSDEGRDCISCKYGGDYSTHNDLLFCRLCTCD 120  
DB 61 LAPQORAPQOKRSSPSGSLCPRGHHSDEGRDCISCKYGGDYSTHNDLLFCRLCTCD 120  
OY 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMKCRKRTGCPRGVAVGDCIPMSDIECVH 180  
DB 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMKCRKRTGCPRGVAVGDCIPMSDIECVH 180  
OY 181 KESGIIIGVTAAVAVLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERVDSSORPGAED 240  
DB 181 KESGIIIGVTAAVAVLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERVDSSORPGAED 240  
OY 241 NVLNEIVSILOPTOVPEQEMEVQEPAPETGVNMLSPGSEHLLPEPAERQORRLVPA 300  
DB 241 NVLNEIVSILOPTOVPEQEMEVQEPAPETGVNMLSPGSEHLLPEPAERQORRLVPA 300  
OY 301 NEGPDETILROCFDFADLVFPDSMEPLMRKLGIMDNEIKAKAEAGHRDTLYTMLIKW 360  
DB 301 NEGPDETILROCFDFADLVFPDSMEPLMRKLGIMDNEIKAKAEAGHRDTLYTMLIKW 360  
OY 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411  
DB 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 11

ABB09602 standard; Protein: 411 AA.

ABB09602;

29-MAY-2002 (first entry)



DE Amino acid sequence of human Apo-2 polypeptide.  
 XX Human: Apo-2, tumour necrosis factor receptor; TNFR; apoptosis;  
 KM caspase; apoptosis; cancer.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..53 /note= "signal peptide"  
 FT Protein 54..411 /note= "mature protein"  
 FT Domain 183..208 /note= "putative transmembrane domain"  
 FT Domain 324..391 /note= "death domain"  
 FT Misc-difference 410 /note= "unspecified amino acid encoded by WTG"  
 FT  
 XX US6342369-B1.  
 XX 29-JAN-2002.  
 XX  
 XX 14-MAY-1998; 98US-0079029.  
 XX  
 XX 15-MAY-1997; 97US-046615P.  
 PR 09-FEB-1998; 98US-074119P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ;  
 XX  
 DR WPI: 2002-224941/28.  
 DR N-PSDB: ABL41729.  
 XX  
 XX New nucleic acids encoding an Apo-2 ligand, useful for activating or  
 PT stimulating apoptosis in cancer cells, thus especially useful in the  
 PT treatment of cancer, or in enhancing immune-mediated cell death -  
 XX  
 PS Example 1; Fig 2A; 68pp; English.  
 XX  
 CC The present sequence represents human Apo-2 polypeptide. It is believed  
 CC that Apo-2 is a member of the tumour necrosis factor receptor (TNFR)  
 CC family. Apo-2 polypeptide is capable of triggering caspase-dependent  
 CC apoptosis and activating nuclear factor-kappa B. A soluble  
 CC extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2l). Apo-2  
 CC antibodies may be used to activate or stimulate apoptosis in cancer  
 CC cells. They are therefore especially useful in the treatment of cancer,  
 CC to enhance immune-mediated cell death in cells expressing Apo-2, to  
 CC detect expression of Apo-2 in specific cells, tissues or serum, and in  
 CC affinity purification of Apo-2 from recombinant cell culture or natural  
 CC sources.  
 CC  
 XX Sequence 411 AA;  
 SO  
 Query Match 99.9%; Score 2167; DB 23; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-178;  
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 KESGIIGTVAAVAVLVAVFVCKSLMKKVLPLYLKICSGGGDPERVDSSQPGAE 240  
 QY 241 NVLNEIYSIIQPTOVPEQNEVOEPAPPTCVNMISPESEHLEPAPAEQSQRLLVPA 300  
 Db 241 NVLNEIYSIIQPTOVPEQNEVOEPAPPTCVNMISPESEHLEPAPAEQSQRLLVPA 300  
 QY 301 NEGDPTETLRQCEFDPAFLVPSWEPMLNRKLGIMDEIKVAKAEAGHSDTYTMLIKW 360  
 Db 301 NEGDPTETLRQCEFDPAFLVPSWEPMLNRKLGIMDEIKVAKAEAGHSDTYTMLIKW 360  
 QY 361 VNKTRDASVHTLLDALETIGERLAKOKIEDHLLSSKFMYLEGNSDAYS 411  
 Db 361 VNKTRDASVHTLLDALETIGERLAKOKIEDHLLSSKFMYLEGNSDAYS 411  
 RESULT 12  
 ABG75645  
 ID ABG75645 standard; Protein; 411 AA.  
 XX  
 AC ABG75645;  
 XX  
 DT 29-APR-2003 (first entry)  
 XX  
 DE Human Tango-63e protein.  
 XX  
 KW Human; inflammation; viral encephalitis; meningitis;  
 KW multiple sclerosis; stroke; Alzheimer's disease; polycythaemia vera;  
 KW hyperproliferative myeloid disease; chronic myelogenous leukaemia;  
 KW HIV infection; autoimmune disease; systemic lupus erythematosus;  
 KW rheumatoid arthritis; type I diabetes; septic shock; graft rejection;  
 KW cerebral malaria; cachexia; cardiovascular disorder; angina pectoris;  
 KW myocardial infarction; hypertension; atherosclerosis;  
 KW hematologic disease; aplastic anaemia; chronic neutropenia;  
 KW myelodysplastic syndrome; Tango-63e; chromosome 8.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US2002160446-A1.  
 XX  
 XX 31-OCT-2002.  
 PD  
 XX 16-MAR-2001; 2001US-0811088.  
 XX  
 XX 14-NOV-2000; 2000US-0712726.  
 PR  
 XX (HOLT/) HOLTZMAN D A.  
 PA (GEAR/) GEARING D P.  
 PA (PANY/) PAN Y.  
 XX  
 PI Holtzman DA, Gearing DP, Pan Y;  
 XX  
 XX WPI: 2003-265758/26.  
 DR N-PSDB: ABX11269.  
 DR  
 XX New isolated nucleic acid molecule encoding thymotaxin (Tango-45),  
 PT Tango-63d, Tango-67e, Tango-67, or huchordin polypeptide, useful for  
 PT diagnosing and treating disorders, e.g. cancer, inflammation, stroke or  
 PT diabetes -  
 XX  
 PS Claim 9; Fig 4; 79pp; English.  
 PS  
 XX The invention relates to an isolated nucleic acid molecule encoding  
 CC thymotaxin (also known as Tango-45), Tango-63d, Tango-637e, Tango-67,  
 CC or huchordin polypeptide, including sequences 90% identical to them,  
 CC fragments of at least 15 nucleotides and allelic variants. Also  
 CC included are a host cell or a non-mammalian host cell containing the  
 CC novel nucleic acid, the encoded polypeptides (or allelic variants,  
 CC sequences 90% identical or fragments), an antibody or antibody  
 CC substance that selectively binds with one of the proteins, and  
 CC identifying a compound that binds with the proteins and/or modulates  
 CC the proteins' activity. Thymotaxin is a member of the C-C family of  
 CC chemokines, Tango-63e and -d are members of the tumour necrosis  
 CC factor superfamily, Tango-67 is a growth factor family member. The

Thymotaxin gene is located on human chromosome 16 and Tango-63 on chromosome 8. The nucleic acid molecules and polypeptides are useful for diagnosing and treating disorders associated with aberrant expression or activity of the nucleic acid or polypeptide, such as inflammation (e.g. viral encephalitis, viral or bacterial meningitis, multiple sclerosis, stroke or Alzheimer's disease), hyperproliferative myeloid disease (e.g. chronic myelogenous leukemia or polycythemia vera), HIV infection, autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis, type I diabetes, septic shock, graft rejection, cerebral malaria or cachexia), cardiovascular disorders (e.g. angina pectoris, myocardial infarction, hypertension or atherosclerosis), or hematologic diseases (e.g. aplastic anaemia, chronic neutropenia or myelodysplastic syndromes). The polypeptides are useful for generating antibodies, which are therapeutically useful. The nucleic acid molecules are useful as primers or probes to detect mutations or polymorphisms in the gene. The methods are useful for identifying compounds that modulate the expression or activity of the polypeptide. The present sequence represents Tango-63e.

Sequence 411 AA;

Query Match 99.9%; Score 2167; DB 24; Length 411;  
Best Local Similarity: 99.8%; Pred. No. 3.3e-178;  
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 MEORGONAPASGARRHGPGRARPGRLRPVKTLYLVAAVLLVSAESALITQOD 60
    |||||
DB 1 MEORGONAPASGARRHGPGRARPGRLRPVKTLYLVAAVLLVSAESALITQOD 60
OY 61 LAPQORAPPOOKRSSPSEGLCPGHHISEDRDICSCKYGODYTHMNDLFLCRLCTCD 120
    |||||
DB 61 LAPQORAPPOOKRSSPSEGLCPGHHISEDRDICSCKYGODYTHMNDLFLCRLCTCD 120
OY 121 SGEVELSCTTTRNTVCCCEGTREEDSPMCRCRCRCRGWVKVGDCTPWSIDICVH 180
    |||||
DB 121 SGEVELSCTTTRNTVCCCEGTREEDSPMCRCRCRCRGWVKVGDCTPWSIDICVH 180
OY 181 KESGIIGVTVAAVLLVAVFCKSLMKKVLPLYLKGISGGGDPREVDSSQRPAGAD 240
    |||||
DB 181 KESGIIGVTVAAVLLVAVFCKSLMKKVLPLYLKGISGGGDPREVDSSQRPAGAD 240
OY 241 NVLNEIYSIILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEPAERSQRRLLVPA 300
    |||||
DB 241 NVLNEIYSIILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEPAERSQRRLLVPA 300
OY 301 NEGPTEFLROCFDPAFLVPDSEWPELMRKLGIMDNIEIKYAKAEAGHRDITLYTMLIKW 360
    |||||
DB 301 NEGPTEFLROCFDPAFLVPDSEWPELMRKLGIMDNIEIKYAKAEAGHRDITLYTMLIKW 360
OY 361 VNKTRGRASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAKS 411
    |||||
DB 361 VNKTRGRASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAKS 411

```

RESULT 13

ABG74383 ID ABG74383 standard; Protein: 411 AA.

XX ABG74383;

XX 11-APR-2003 (first entry)

XX Human TNFR family related protein Apo-2.

XX Human: apo-2; tumour necrosis factor family; TNFR; gene therapy;

XX apoptosis; tissue-specific typing; affinity purification;

XX Competitive-type receptor binding assay.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Domain 1..182

FT Domain /label= Extracellular\_domain\_1  
FT 54..182  
FT /label= Extracellular\_domain\_2  
FT Domain 324..391  
FT /label= Isolated\_death\_domain  
FT Misc-difference 410  
FT /note= "Encoded by WTG"

US2002150985-A1.

17-OCT-2002.

02-NOV-2001; 2001US-0052798.

15-MAY-1997; 97US-046615P.

09-FEB-1998; 98US-074119P.

14-MAY-1998; 98US-0079029.

(GERTH ) GENENTECH INC.

Adams CW, Ashkenazi AJ, Chuntharapal A, Kim KJ;

WPL; 2003-198287/19.

N-PSDB; ABX16403.

New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, or in generating antibodies against Apo-2.

Claim 4; Fig 1A-C; 64pp; English.

The invention describes a novel isolated Apo-2 polypeptide. The Apo-2 polypeptide is useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, as a control against samples containing unknown techniques of Apo-2, in generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays when labeled with, for instance, radiolodine, enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a diagnostic for tissue-specific typing. This is the amino acid sequence of the novel Apo-2 protein of the invention, thought to be a member of the tumour necrosis factor receptor (TNFR) family.

Sequence 411 AA;

Query Match 99.9%; Score 2167; DB 24; Length 411;  
Best Local Similarity: 100.0%; Pred. No. 3.3e-178;  
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MEORGONAPASGARRHGPGRARPGRLRPVKTLYLVAAVLLVSAESALITQOD 60
    |||||
DB 1 MEORGONAPASGARRHGPGRARPGRLRPVKTLYLVAAVLLVSAESALITQOD 60
OY 61 LAPQORAPPOOKRSSPSEGLCPGHHISEDRDICSCKYGODYTHMNDLFLCRLCTCD 120
    |||||
DB 61 LAPQORAPPOOKRSSPSEGLCPGHHISEDRDICSCKYGODYTHMNDLFLCRLCTCD 120
OY 121 SGEVELSCTTTRNTVCCCEGTREEDSPMCRCRCRCRGWVKVGDCTPWSIDICVH 180
    |||||
DB 121 SGEVELSCTTTRNTVCCCEGTREEDSPMCRCRCRCRGWVKVGDCTPWSIDICVH 180
OY 181 KESGIIGVTVAAVLLVAVFCKSLMKKVLPLYLKGISGGGDPREVDSSQRPAGAD 240
    |||||
DB 181 KESGIIGVTVAAVLLVAVFCKSLMKKVLPLYLKGISGGGDPREVDSSQRPAGAD 240
OY 241 NVLNEIYSIILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEPAERSQRRLLVPA 300
    |||||
DB 241 NVLNEIYSIILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEPAERSQRRLLVPA 300
OY 301 NEGPTEFLROCFDPAFLVPDSEWPELMRKLGIMDNIEIKYAKAEAGHRDITLYTMLIKW 360
    |||||
DB 301 NEGPTEFLROCFDPAFLVPDSEWPELMRKLGIMDNIEIKYAKAEAGHRDITLYTMLIKW 360

```

QY 361 VNKTGRDASVHTLLDALLETGERLAKOKIEDHLLSSGKFMYLEGNDASXS 411  
|||||  
Db 361 VNKTGRDASVHTLLDALLETGERLAKOKIEDHLLSSGKFMYLEGNDASXS 411

RESULT 14  
ID AAM93576 standard; Protein; 411 AA.  
AC AAM93576.  
XX  
XX 18-JUN-1999 (first entry)  
XX  
XX Human hAPO8 protein.  
DE

KM Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;  
KM developmental abnormality; gestational abnormality; prostate cancer;  
KM APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;  
KM cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;  
KM apoptosis; human.  
XX  
XX Homo sapiens.  
OS  
XX  
XX W09911791-A2.  
XX  
XX 11-MAR-1999.  
PD  
XX  
XX 04-SEP-1998; 98MO-US18393.  
PF  
XX  
XX 05-SEP-1997; 97US-0924634.  
PR  
XX  
XX (UNIM ) UNIV WASHINGTON.  
XX  
XX  
XX Chaudhary PM;  
PI  
XX  
XX WPI; 1999-205191/17.  
DR  
XX  
XX N-PSDB; AAX23410.  
DR

PT New Tumor Necrosis Factor family receptor polypeptides and ligands -  
PT useful for diagnosis and treatment of prostate cancer and  
PT developmental or gestational abnormalities  
XX  
XX  
XX Claim 19; Fig 2; 156pp; English.  
PS

CC This invention describes isolated Tumor Necrosis Factor (TNF) family  
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active  
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or  
CC their active fragments. APO4 is useful for diagnosing prostate cancer  
CC by determining levels of APO4 in an individual. Prostate cancer can also  
CC be treated using APO4 selective binding agents linked to a therapeutic  
CC moiety. APO4 polypeptides are also useful for identifying selective  
CC binding agents, useful in diagnosis/treatment of disease by binding of  
CC agents to the polypeptide/active fragment which is extracellular, or  
CC expressed on the cell surface. The binding is preferably performed in  
CC vivo. APO4 polypeptides/active fragments are also useful for screening  
CC for agonists and antagonists by binding and observing the change in APO4  
CC activity. Effective pharmacological agents useful in diagnosis or  
CC treatment of disease are also identified using APO4 polypeptides/active  
CC fragments and APO4 signal transducer molecules that specifically interact  
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4  
CC activity. The method is performed in vivo or in vitro. APO polypeptides  
CC are all useful as immunogens for preparing antibodies. APO4 is also  
CC useful for diagnosis/treatment of developmental or gestational  
CC abnormalities. APO8 was transfected to human breast carcinoma cell line  
CC MCF-7, and induced apoptosis.  
CC  
XX  
XX  
XX

SQ Sequence 411 AA;  
Query Match 99.7%; Score :163; DB 20; Length 411;  
Best Local Similarity 99.5%; Pred. Ho. 7.2e-178;  
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEORGNAPAPASGARRHGPGPREAR(ARPGLRVPTLVVAVALLVSAESALITQOD 60

Db  
1 MEORGNAPAPASGARRHGPGPREAR(ARPGLRVPTLVVAVALLVSAESALITQOD 60  
|||||

QY 61 LAPQORAPAPQOKRSSSEBEGICPPGHHISEGRCISCKYGODYSTHWNDLPLCLRCTRD 120  
|||||

Db 61 LAPQORAPAPQOKRSSSEBEGICPPGHHISEGRCISCKYGODYSTHWNDLPLCLRCTRD 120  
|||||

QY 121 SGEVELSPCTTNTNTYCCQCEBEGTFREDESPKCRKRTGCPKGMVVGCTPMSDIECVH 180  
|||||

Db 121 SGEVELSPCTTNTNTYCCQCEBEGTFREDESPKCRKRTGCPKGMVVGCTPMSDIECVH 180  
|||||

QY 181 KESGIIIGVTAAVVLAIVAFVCKSLMKVLPYLKIGSGGGGDEPVRDSSQRGABD 240  
|||||

Db 181 KESGIIIGVTAAVVLAIVAFVCKSLMKVLPYLKIGSGGGGDEPVRDSSQRGABD 240  
|||||

QY 241 NVNTEIVSILOPVOPEQOEVEQEPAPPTGCVNMLSGESHLLEPAEERSQRRLLVPA 300  
|||||

Db 241 NVNTEIVSILOPVOPEQOEVEQEPAPPTGCVNMLSGESHLLEPAEERSQRRLLVPA 300  
|||||

QY 301 NEGDPFETLRQCFDDPADLVPPFDSWPELMKRLGLMONEIKVAKAEAGHRDLYTMLIKW 360  
|||||

Db 301 NEGDPFETLRQCFDDPADLVPPFDSWPELMKRLGLMONEIKVAKAEAGHRDLYTMLIKW 360  
|||||

QY 361 VNKTGRDASVHTLLDALLETGERLAKOKIEDHLLSSGKFMYLEGNDASXS 411  
|||||

Db 361 VNKTGRDASVHTLLDALLETGERLAKOKIEDHLLSSGKFMYLEGNDASXS 411  
|||||

RESULT 15  
ID AAY00932 standard; Protein; 411 AA.  
AC AAY00932.  
XX  
XX AAY00932;  
XX  
XX 02-JUN-1999 (first entry)  
XX  
XX Human DR5 protein sequence.  
DE  
XX  
XX Human; DR5; TRAIL-R3; apoptosis related condition; cancer; therapy;  
XX autoimmune disease; viral infection; degenerative disorder;  
XX amyotrophic lateral sclerosis; retinitis pigmentosa; ischemic injury;  
XX cerebellar degeneration; myelodysplastic syndrome.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX W09909165-A1.  
XX  
XX 25-FEB-1999.  
PD  
XX  
XX 14-AUG-1998; 98MO-US16945.  
PF  
XX  
XX 15-AUG-1997; 97US-0055906.  
PR  
XX  
XX (IDUN-) IDUN PHARM INC.  
XX  
XX  
XX Alnemir ES;  
PI  
XX  
XX WPI; 1999-181035/15.  
DR  
XX  
XX N-PSDB; AAX27279.  
DR

PT Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
PT protein - useful in for screening for (ant)agonists that modulate  
PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
XX  
XX  
XX Claim 16; Page 58-60; 71pp; English.  
PS

CC This sequence is the human TRAIL receptor DR5 of the invention. An  
CC antibody against the TRAIL receptors is useful for detecting mammalian  
CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
CC (ant)agonists identified by the assay are useful for modulating the  
CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
CC related conditions which are treated in this way. Include cancer

